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OM nucleic - nucleic search, using sw model

Run on: January 23, 2002, 18:42:32 ; Search time 1581.67 Seconds

(Without alignments)  
10492.810 Million cell updates/sec

Title: US-09-453-387A-1  
Perfect score: 1006  
Sequence: 1 taacacgcgtatctcttc.....aatgcttaattataaaaa 1006

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl1:  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_om:\*  
20: em\_or:\*  
21: em\_ov:\*  
22: em\_pat:\*  
23: em\_ph:\*  
24: em\_pl:\*  
25: em\_ro:\*  
26: em\_sts:\*  
27: em\_sy:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htgo\_hum:\*  
31: em\_htgo\_hum:\*  
32: em\_htgo\_rod:\*  
33: em\_htg\_hum:\*  
34: em\_htg\_inv:\*  
35: em\_htg\_rod:\*  
36: em\_htg\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1006	100.0	1006	8	COTMYBA	L04497 Cotton DNA-
2	282.4	28.1	1145	8	AF336286	U26336 Gossypium
3	263.8	26.2	764	8	ATU26336	U26336 Arabidopsis
4	254.2	25.3	1152	8	LETM27	X95296 L. esculentu
5	253.6	25.2	639	8	AF207991	AF207991 Arabidops
6	248	24.7	1003	8	AF062860	AF062860 Arabidops
7	242.4	24.1	897	8	AF062859	U26337 Arabidops
8	234.6	23.3	844	8	ATU26337	U26337 Arabidops
9	217	21.6	1151	8	AF034134	AF034134 Gossypium
10	216.4	21.5	1284	8	HVMYB1	X70877 H. vulgare m
11	206.8	20.6	1176	8	D88617	D88617 Oryza sativ
12	205.6	20.4	1102	8	HVMYB2	X70876 H. vulgare m
13	201	20.0	1066	8	D88618	D88618 Oryza sativ
14	194.2	19.3	1335	8	ATCMXGENE	X90382 Arabidops
15	189.2	18.8	1118	8	ATMIXTA	X79108 A. majus mix
16	189	18.7	1337	8	LETM16	X92910 L. esculentu
17	187.8	18.7	1493	8	AF062916	AF062916 Arabidops
18	187.4	18.6	1135	8	AF401220	AF401220 Fragaria
19	186.6	18.5	984	8	AF175990	AF175990 Arabidops
20	186	18.5	1364	8	AB005889	AB005889 Arabidops
21	185.6	18.4	795	8	AB029160	AB029160 Glycine m
22	183	18.2	966	8	AF249310	AF249310 Arabidops
23	183	18.2	991	8	AF336285	AF336285 Gossypium
24	182.8	18.2	795	8	AB029161	AB029161 Glycine m
25	181.8	18.1	1588	8	PHMYBPH31	Z13996 P. hybrida m
26	180.2	17.9	1148	8	AF386932	AF386932 Arabidops
27	179.2	17.8	960	8	AF175991	AF175991 Arabidops
28	178.6	17.8	1002	8	AF371983	AF371983 Arabidops
29	178.6	17.8	1038	8	AF249309	AF249309 Arabidops
30	176.2	17.5	1220	8	AF161711	AF161711 Plumbagin
31	176	17.5	1332	8	AWA6292	AJ0006292 Antirrhin
32	175	17.4	1252	8	ATMIXTA	X99809 A. Thaliana
33	174.8	17.4	1032	8	LETM18GE	X98308 L. esculentu
34	174.4	17.3	819	8	AB029165	AB029165 Glycine m
35	174.2	17.3	1022	8	AF062869	AF062869 Arabidops
36	174.2	17.3	1462	8	PMO38448	U39448 Picea maria
37	174.2	17.3	1612	8	AY035145	AY035145 Arabidops
38	172.4	17.1	1101	8	AF175998	AF175998 Arabidops
39	171.6	17.1	1292	8	AF062872	AF062872 Arabidops
40	171	17.0	981	8	AF370613	AF370613 Arabidops
41	170.6	17.0	113800	8	AC006567	AC006567 Arabidops
42	170.6	17.0	197394	8	ATCHRIV27	AL161515 Arabidops
43	169.8	16.9	1384	8	AF062887	AF062887 Arabidops
44	169.2	16.8	1017	8	AF175992	AF175992 Arabidops
45	168	16.7	828	8	AB029162	AB029162 Glycine m

## ALIGNMENTS

RESULT 1  
LOCUS COTMYBA 1006 bp mRNA  
DEFINITION Cotton DNA-binding domain mRNA.  
ACCESSION L04497  
VERSION L04497.1 GI:437326  
KEYWORDS  
SOURCE Gossypium hirsutum (cultivar Acala Sf-2) 3-day pre-anthesis ovule  
CDNA to mRNA.

## ORGANISM

Gossypium hirsutum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eustosids II; Malvales; Malvaceae; Gossypium.

REFERENCE 1 (bases 1 to 1006).  
AUTHORS Wilkins, T. A. and Lu, C.-C.

## JOURNAL

Unpublished

## FEATURES

Location/Qualifiers  
1..1006  
/organism="Gossypium hirsutum"  
/cultivar="Acala Sf-2"

Query Match	Score	DB	Length
Best Local Similarity	80.3%	Pred	No. 2.4e-63;

Matches	331	Conservative	0	Mismatches	81	Indels	0	Gaps	0
Qy	39	ttgattgaattt	gttaactgatyggagacatacactt	gttgytaaaaggtctataccaaca	98				
Db	49	TTTCTTTGTGTACTGATTAATGGAAGGTCTCCTTGTGTGAGAAAGCTCATACGACA	108						
Qy	99	aaggtgctctgaaaccaagaagaagatacaagccatacaactacatcgtytccatgtyt	158						
Db	109	AAGGTGCGTGGCTTAAGAAAGAAAGATGATCCGCTCATAGCTTACATCCAGAGCCCATGATG	168						
Qy	159	aaggtcgtctgagcttccctccccaagctgctgcctggagctgttagatgtytgaagtgtga	218						
Db	169	AAGGTGCTGGGTGTCACTCCCTTAAGGTGCTGGGCTTCTCCGCTGTGGCAAAAGTTGTA	228						
Qy	219	gattaaagtgtataaacacttgaagcgctgatacttaagagbagaatttcactgaagaag	278						
Db	229	.GACTTCGTTGGTCACTAATTAAACCTGATCTTAAGTGGCAATTCACTGAAAGAG	288						
Qy	279	aagatgagctctatcaaacgtctcaagcttactcttggaaacaaatggtcatgattgcty	338						
Db	289	AAGATGACCTCTTATTCAGCTGCACAGCGCTTCTTGTTAAACAAGTGGTCTTATTAAGCGG	348						
Qy	339	gaagattcccaaggaagacagataatgagataaagaactctggaaacacacacatcaaa	398						
Db	349	GGAGATTTCAGGAAGAAACAGTAAATGAGATTAAAGATTAATCTGGAAACGCCATATAGAA	408						
Qy	399	gaagactataagcagaggaatttgataccacaacatcatcgtctctctcaatca	450						
Db	409	GGAAGCTTTAGCGCAGAGTATGTATGCCAGCACTACAGCGCCACTCAATGA	460						

RESULT	3
LOCUS	ATU26936
DEFINITION	Arabidopsis thaliana clone myb6 DNA-binding protein mRNA, complete cds.
ACCESSION	U26936
VERSION	U26936.1
SOURCE	G1:1020154
ORGANISM	thale cress. Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsiss.
REFERENCE	1 (bases 1 to 764) Li,S.F. and Parish,R.W. Isolation of two novel myb-like genes from Arabidopsis and studies on the DNA-binding properties of their products Plant J. 8 (6), 963-972 (1995)
AUTHORS	2 (bases 1 to 764) Heazlewood,J.L. Direct Submission Submitted (12-MAY-1995) Joshua L. Heazlewood, Botany, La Trobe University, Melbourne, Victoria 3083, Australia
JOURNAL MEDLINE TITLE	Location/Qualifiers
FEATURES	1..764 /organism="Arabidopsis thaliana" /strain="Landsberg erecta" /db_xref="taxon:3702" /clone="myb6" 15..725 /codon_start=1 /product="DNA-binding protein" /protein_id="AA98761.1" /db_xref="G1:1020155"
CDS	/translation="MGRSPCCERAKHTNGAWTKEDORLVYDIIRNHGGCWRSLPKSGILRGCSRLRMIVYLRPDLCKRNFTEDEQIILKLSLGKKWSLIAGRLPGRTGLTETEKNNWNIHKRIKLSHGIDPOTHRINSCTVSSOVVYIONDAVSFNSLAVKKTENSDNASTGTGTTDELDRNGCEGYDGNSHIKLNLDLTLLTGFSMSRRIYGVGSADSKRWCPDYMARISLT."
BASE COUNT	228 A 140 C 177 G 219 T
ORIGIN	

Query Match	26.2%	Score 263.8	DB 8	Length 764
Best Local Similarity	79.2%	Pred. No. 1.7e-58		
Matches 313	Conservative 0	Mismatches 82	Indels 0	Gaps 0
QY 59	atggagcagatcaacctgtgtgtgaaaaggctcataccacaagaagtgcctcgagccaagaag			118
Db 15	ATGGGAAGATCCTCGTTGTGAAAAAGCTCACAAAAAAGAGAGCTTGACCTAAAGNA			74
QY 119	gaagataaagccctcatcaactaactcgcgtgcctcgttgtaaggatgctgagctccccc			178
Db 75	GAAATCAACCTCTCGTAGATTATATCCGTATATCCGGTGAAGGTTGTGGCTTCTCTT			134
QY 179	cccaagctgctgggctgctcttagatgtgtgtaagatttcagaattaaatgtgtaaaactac			238
Db 135	CCTAAATCCCGTGGATTGTTCGCTGTGTGTAATAAGTTGAGATTGATGATTAATTATAC			194
QY 239	ttagagcctgactctctaagagaagaaattcaactgaagaagaatgagactctatctcaag			298
Db 195	CTTGCTCTGTATCTTTAAACGTGTATATTTACTGTATGATGAAGATCAATCATCAAAA			254
QY 299	cttcacagtttaactgtggaacaacatggtcatgtatctgtctgagaatactccagaagaaca			358
Db 255	CTCCATAGCTTACACGCGTAACAAATAGGTCATTGATAGCTGGAAAGTTTACACGAAAGACA			314
QY 359	gataatgagataaagaactacttggaaacacacacatcaaaagaagaactataagcagaaga			418
Db 315	GATTAACGAAATTAAGAAATTATTGAAACATCTATTATTAAGAGCAACCTTTAGTACGGT			374
QY 419	atgatgcacaacactcatgcctctcctcaatcaaac	453		
Db 375	ATTGATCCACAAACTCATGTCAGATTTAACGATC	409		

RESULT		4	
LETHM27			
LOCUS	LETHM27	1152 bp	mRNA
DEFINITION	L.esculentum mRNA for THM27 protein.		
ACCESSION	X95296		
VERSION	X95296.1	GI:1167483	
KEYWORDS	myb-related gene; THM27 gene; transcription factor. tomato.		
ORGANISM	Lycopersicon esculentum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots; Asterridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 1152) Lin,O., Hamilton,W.D. and Merryweather,A. Cloning and initial characterization of 14 myb-related cDNAs from tomato (Lycopersicon esculentum cv. Alisa Craig)		
TITLE			
JOURNAL	Plant Mol. Biol.	30 (5),	1009-1020 (1996).
MEDLINE	96270378		
REFERENCE	2 (bases 1 to 1152) Lin,O.		
AUTHORS	Direct Submission		
TITLE	Submitted (23-JAN-1996) Q. Lin, John Innes Centre, Colney Lane,, Norwich, NR4 7UH, UK		
JOURNAL			
FEATURES	Location/Qualifiers 1..1152 /organism="Lycopersicon esculentum" /cultivar="Alisa Craig" /db_xref="taxon:4081" /dev_stage="3 weeks old seedling" /tissue_type="hypocotyl" 111..932 /gene="THM27" 111..932 /gene="THM27" /note="myb-related" /codon_start=-1 /product="transcription factor"		
CDS			
gene			





LOCUS	ATU26937	844 bp	mRNA	PLN	03-MAY-1996
DEFINITION	Arabidopsis thaliana clone myb7 DNA-binding protein mRNA, complete cds.				
ACCESSION	U26937				
VERSION	U26937.1 GI:1020156				
KEYWORDS	thale cress.				
SOURCE	Arabidopsis thaliana				
ORGANISM	Eunaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
REFERENCE	1 (bases 1 to 844)				
AUTHORS	Ll.S.F. and Parish,R.W.				
TITLE	Isolation of two novel myb-like genes from Arabidopsis and studies on the DNA-binding properties of their products				
JOURNAL	Plant J. 8 (6), 963-972 (1995)				
MEDLINE	96132152				
REFERENCE	2 (bases 1 to 844)				
AUTHORS	Heazlewood,J.L.				
TITLE	Direct Submission				
JOURNAL	Submitted (12-MAY-1995) Joshua L. Heazlewood, Botany, La Trobe University, Melbourne, Victoria 3083, Australia				
FEATURES	Location/Qualifiers				
source	1..844				
	/organism="Arabidopsis thaliana"				
	/strain="Landsberg erecta"				
	/db_xref="taxon:3702"				
	/clone="myb7"				
	12..821				
	/codon_start=1				
	/product="DNA-binding protein"				
	/protein_id="AA98763.1"				
	/db_xref="GI:1020157"				
	/translation="MGKSPCCCKEHMKNGKANTKEEDRLYSIKSHGECNRSLPRRAFLGLKGRSGRLRWNTNLRPDLKRGNTFHDEDELIKLHSLGNKWSLTAARLPGRTDIEIKNYWTHIRKRLKLSGIDPATRGHINEAKISDLKTKDDIVDVSPTKFEETDKGDQONKYIRNGLCKEERYYEERIKGIDPLELIERISPPMONOEISCTCSFRFMEEMDCESEYVACQFNSSSISVSSIDISSNNGYDFLGRKILDPRLSEMK"				
BASE COUNT	289 a 137 c 200 g 218 t				
ORIGIN					
Query Match	23.3%; Score 234.6; DB 8; Length 844;				
Best Local Similarity	74.8%; Pred. No. 7.8e-51;				
Matches 294;	Conservative 0; Mismatches 99; Indels 0; Gaps 0;				
Db	55	actgatggagagatcattctgttgtgaaaagctatcccaagaagtgcctgacc	114		
Db	8	AGTCATGGGAAGATCTCTTGCTGCGAAGAAAGAACACATGAACAAAGGCTTGAC	67		
QY	115	agaggaagatcaacagcccatcaactacatccggtgcatggtgtaaggctgcgtgc	174		
Db	68	AGAAGAAATGAGAGACTAGTCTCTTACATCAAGCTCACGGTGAAGGTGTGGCGATC	127		
QY	175	ctctcccaaaagctgctggtgctgtatagtgtgtaagaagctgcagattaagaataa	234		
Db	128	TCTTCTCTGAGACCCGCTGGTCTCTTCCTTCGCTGGGGTAAAGCTGCCTCTTCGGTG	187		
QY	235	ctacttgagagctgctcttaagagagagaattcaactgaagaagagatagcttatcat	294		
Db	188	CTATCTCGGACTGATCTTCAAAGAGGAACTTTCACATGATGAGATGAACCTTATCT	247		
QY	295	caagctcaagcttacttggaaacaatggtgcattgattgctgtgaagaattaccagaag	354		
Db	248	CAAGCTCATATGACCTCTCAGCAACAAAGTGGCTTTGATTGGCGGAGATTACCTGAAG	307		
QY	355	aacagataaagataaagaactacttgaaacacacactcaaaaagaagcttatagaag	414		
Db	308	AACGATACGAGATCAAGAACTATGTGAAACACATATTAAGAGGAAGCTTTGACCA	367		

QY	415	agaagtgtatccacaactcatgcctctccaa	447
DB	368	agcgatgtatccagccactcatgagagatcaa	400
RESULT	9		
LOCUS	AF034134	1151 bp	MRNA
DEFINITION	Gossypium hirsutum MYB-like DNA-binding domain protein (Cmy-O)		02-MAR-1998
ACCESSION	AF034134		
VERSION	AF034134.1	GI:2921339	
KEYWORDS			
SOURCE	upland cotton.		
ORGANISM	Gossypium hirsutum		
REFERENCE	Eunaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.		
AUTHORS	1 (bases 1 to 1151)		
TITLE	Loguercio, L.L., Zhang, J. and Wilkins, T.A.		
JOURNAL	Structure and expression of six classes of myb-domain genes in allotetraploid cotton (Gossypium hirsutum L.)		
REFERENCE	2 (bases 1 to 1151)		
AUTHORS	Loguercio, L.L., Zhang, J. and Wilkins, T.A.		
TITLE	Direct Submission		
JOURNAL	Submitted (13-NOV-1997) Agronomy & Range Science, University of California, One Shields Ave., Davis, CA 95616-8515, USA		
FEATURES			
source	1..1151		
gene	/organism="Gossypium hirsutum"		
	/cultivar="Acala, Sf-2"		
	/db_xref="taxon:3635"		
	/dev_stage="3 days pre-anthesis"		
	/tissue_type="ovule"		
	1..1151		
	/gene="Cmy-O"		
	/note="MYB-domain gene O"		
CDS	72..752		
	/gene="Cmy-O"		
	/function="putative MYB-like transcription factor"		
	/note="similar to MYB A encoded by Genbank Accession Number U04497"		
	/codon_start=1		
	/product="MYB-like DNA-binding domain protein"		
	/protein_id="AAC04720.1"		
	/db_xref="GI:2921340"		
	/translation="MRPCCDCKGTNGAMSKQEDKLDYIRIHGECMRLPKPAAGLHRCGSKRLRWLVLPDRIKGNFAODEEDLIRLHLILGNRWSLIGRPGRTDNNVKNWNSHKIRKLKMGIDIPNHRKLNQYRHHVGLNPLPTTMSDVACKLRCSNDNDIGISPAATLEATPTPTGISNLDLDTLTFSPSPKNIIEEQATASIVYNDDEEQYTVPTLRLR"		
	102..257		
	/note="putative MYB DNA-binding domain repeat R2"		
	258..412		
	/note="putative MYB DNA-binding domain repeat R3"		
BASE COUNT	362 a 215 c 240 g 314 t		
ORIGIN			
Query Match	21.6%	Score 217;	DB 8; Length 1151;
Best Local Similarity	71.3%	Pred. No. 3.3e-46;	
Matches	286; Conservative	0; Mismatches 115;	Indels 0; Gaps 0;
QY	36	gattgatttgaatttgttaactgatggaagatcaccttgytgytaaaagcgtacaca	95
DB	46	gtttacttttgatttgaatttgaactccgagagcgaacaccttgcgcgatataacacagcaccaca	105
QY	96	acaagaagtgctgagcaccagaagagatcaacgctcatcaactacacgcgtgcctcat	155
DB	106	acaaaggagccctggtccaaagcagaagatcaaaacacctcatgattatattacgtattcatng	165

BASE COUNT	320 a	399 c	363 g	202 t
ORIGIN				
Query Match	21.5%;	Score 216.4;	DB 8;	Length 1284;
Best Local Similarity	71.8%;	Pred. No. 4.8e-46;		
Matches 283; Conservative	0;	Mismatches 111;	Indels 0;	Gaps 0;
OY	54	aacgatgggaagcgtcaacctggttgytaaaaggtctatccaacaagaagtccctygacca	113	
Db	207	AAGCGATGGGAGGTCCGCTGCTCGCAGNAGGGGCACCAACAAGGCCCTCGAGCCA	266	
OY	114	aagaaggaaatcaaacgcctcatcacactaccgtylccatgtytgaaagctgctygcgt	173	
Db	267	AGGAGGAGGAGACGACCAGTCAACGCCCTACATCAAGAGGCCACGCGAGGCGTGCGCGCT	326	
OY	174	ccttcgccaaaagctgctygcgtgcttagatgtygtgtaaagttgcagattaagatgataa	233	
Db	327	CCCGGCCAAGCGCGCGCGCTGCTCGCGTCGCGCAMAAGATGCGCGCTCGCGTGATCA	386	
OY	234	actacttgagagcctgattcttaagaagagaaatctcaacgcyaagaagaatgatattaca	293	
Db	387	ACTACTCTCCGCCCGCACCTCAAGCGCGCAACTTCAGCCACGAGAGAGACGACGCTCATCA	446	
OY	294	tcaagcttcacagttacttcttgaaacaatatggtcatgtattgctcygaagattaccaggaa	353	
Db	447	TCAAAGCTCAACAGCTCCTCGGGAATAAAATGTGCTCTATATAGCGGGAGACTGCGCGGGA	506	
OY	354	gaacagataatgagataaagaactactcygaacacacacacataaagaagacttatagca	413	
Db	507	GGACGCAACAGAGATCAAGAATCTACTGGAACACGACATCCGGAGGAAGCTGACGAGCC	566	
OY	414	gaggaatgatccacaactcatgtctcttcaa	447	
Db	567	GGGGATGACCCGGGTGACCCACCGCGGATCA	600	
RESULT 11				
LOCUS	D88617	1176 bp	mRNA	PLN
DEFINITION	Oryza sativa mRNA for OSMYB1, complete cds.			
ACCESSION	D88617			
VERSION	D88617.1	GI:2605616		
KEYWORDS	OSMYB1; OSMYB1.			
SOURCE	Oryza sativa seed cDNA to mRNA.			
ORGANISM	Oryza sativa			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
AUTHORS	Sphenaclophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
TITLE	Epharoidaeae; Oryzeae; Oryza.			
JOURNAL	1 (bases 1 to 1176)			
REFERENCE	Suzuki,A.			
AUTHORS	Direct Submission			
TITLE	Submitted (28-OCT-1996) to the DBU/EMBL/GenBank databases. Akhtir			
JOURNAL	Suzuki, National Institute of Agrobiological Resources, Department			
REFERENCE	of Biotechnology; Kannondai 2-1-2, Tsukuba City 305, Japan			
AUTHORS	(E-mail:hnskhk@abrr.affrc.go.jp, Tel:+81-298-38-8450,			
FEATURES	Fax:+81-298-38-8397)			
FEATURES	2 (sites)			
REFERENCE	Suzuki,A., Suzuki,T., Tanabe,F., Toki,S., Washida,H., Wu,C.Y. and			
AUTHORS	Takaiwa,F.			
TITLE	Cloning and expression of five myb-related genes from rice seed			
JOURNAL	Gene 198 (1-2), 393-398 (1997)			
MEDLINE	98036074			
FEATURES	Location/Qualifiers			
FEATURES	1..1176			
FEATURES	/organism="Oryza sativa"			
FEATURES	/db_xref="taxon:4530"			





RESULT	13
LOCUS	D88618 1069 bp mRNA PLN 07-FEB-1999
DEFINITION	Oryza sativa mRNA for OSMYB2, complete cds.
ACCESSION	D88618
VERSION	D88618.1 GI:2605618
KEYWORDS	Osmyb2; OSMYB2.
SOURCE	Oryza sativa seed cDNA to mRNA.
ORGANISM	Oryza sativa
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzaceae; Oryza.
AUTHORS	1 (bases 1 to 1069)
JOURNAL	SUZUKI, A.
REFERENCE	Direct Submission
AUTHORS	Submitted (28-OCT-1996) to the DDBJ/EMBL/GenBank databases. Akihito Suzuki, National Institute of Agrobiological Resources, Department of Biotechnology, Kanondai 2-1-2, Tsukuba City 305, Japan (E-mail:mskirk@ab.affrc.go.jp, Tel:+81-298-38-8450, Fax:+81-298-38-8397)
FEATURES	2 (sites)
FEATURES	Suzuki, A., Suzuki, T., Tanabe, F., Toki, S., Washida, H., Wu, C. Y. and Takaiwa, F.
FEATURES	Cloning and expression of five myb-related genes from rice seed Gene 198 (1-2), 393-398 (1997)
FEATURES	98036074
FEATURES	Location/Qualifiers
FEATURES	1..1069
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167	GGAGGACCGCCCTCATCGCCACATCCACACAGCAGCGCGGAGGGCTGTGGAGTGGCT 226
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RESULT	14			
LOCUS	ATMG4ENE	1335 bp	mRNA	PLN
DEFINITION	Arabidopsis thaliana mRNA for putative transcription factor (MYB102 gene).			
ACCESSION	X90382			
VERSION	X90382.2	GI:7263578		
KEYWORDS	myb-repeat; MYB102 gene; transcription factor.			
SOURCE	thale cress.			
ORGANISM	Arabidopsis thaliana			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.			
AUTHORS	1 (bases 1 to 1335) Quaedvlieg,N., Dockx,J., Keultjes,G., Kock,P., Wilmering,J., Weisbeek,P. and Smeekens,S.			
TITLE	Identification of a light-regulated MYB gene from an Arabidopsis transcription factor gene collection			
JOURNAL	Plant Mol. Biol. 32 (5), 987-993 (1996)			
MEDLINE	97134989			
REFERENCE	2 (bases 1 to 1335)			
AUTHORS	Keultjes,G.G.M.			
JOURNAL	Direct Submission			
REMARK	Submitted (28-JUL-1995) G.G.M. Keultjes, University of Utrecht,			
REFERENCE	Paduaan 8, 3584 CH Utrecht, NETHERLANDS			
AUTHORS	Revised by [3]			
TITLE	3 (bases 1 to 1335)			
JOURNAL	Smeekens,J.C.M.			
REMARK	Direct Submission			
AUTHORS	Submitted (17-MAR-2000) Smeekens J.C.M., Molecular Plant			
TITLE	Physiology, Utrecht University, Paduaan 8, 3584 CH Utrecht, The			
JOURNAL	Netherlands			
COMMENT	On Mar 19, 2000 this sequence version replaced g1:928927.			
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PD 07-JUN-2001.



XX	AC	XX	AAc49989;	XX
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XX	KM	XX	Hybridisation assay; genetic mapping; gene expression control	XX
XX	KW	XX	protein identification; signal transduction pathway;	XX
XX	XX	XX	metabolic pathway; promoter; termination sequence; ss	XX
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PD	06-SEP-2000.			
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PF	25-FEB-2000; 2000EP-0301439.			
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Query Match	26.2%;	Score 263.8;	DB 21;	Length 871
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Oy	239	ttagagcctatccttaagagaganaattcatactgaagaagaatgaagcttatcatcaag	298						
Db	234	cttcgtctcgtatccttaaacgttgtaattctcatgatgatgaagctcaatcatcatcaa	293						
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DT	25-JAN-2001	(first entry)							
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XX		Plant; transcription factor; gene expression; eucalyptus; pine; acacia;							
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KM		homeodomain zipper; LIM domain; AP2; ERBBS; zinc finger domain;							
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DR	WPI; 2000-579369/54.								
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PT	New isolated polynucleotide encoding a plant transcription factor for								
PT	producing a plant e.g. a woody plant, preferably eucalyptus or pine,								
PT	having modified gene expression or modified activity of a polypeptide								
PS									
XX									
CC	Claim 1; Page 653; 747pp; English.								
XX	The present invention relates to novel plant transcription factors from								



**Sequence** 473 BP; 131 A; 134 C; 120 G; 88 T; 0 other;

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 Db 155 cgtctcccaagcgcgcagggctgtctctgagaatgcgcgaagagcttgcagagctgcgtatgataa 214

[illegible]

XX	RESULT	6
XX	AAC57075	
ID	AAC57075	standard; DNA; 509 BP.
XX		
XX	AAC57075;	
XX		
DT	25-JAN-2001	(first entry)
XX		
De	Plus radiata transcription factor DNA sequence #521.	
XX		
KW	Plant; transcription factor; gene expression; eucalyptus; pine; acacia;	
KW	poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor;	
KW	basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;	
KW	homeodomain zipper; LIM domain; AP2; EREBS; zinc finger domain;	
KW	type 2 Cys2His2; CCAAT box element; MYB; ss.	
XX		
OS	Plus radiata.	
XX		
PN	WO200053724-A2.	
XX		
PD	14-SEP-2000.	
XX		
PF	09-MAR-2000; 2000WO-US06112.	
XX		
PR	11-MAR-1999; 99US-0266513.	

DR WPI; 2000-579369/54.

XX  
PS C:\ajm 1: Page 580: English

CC The present invention relates to novel plant transcription factors from  
CC Eucalyptus grandis or Pinus radiata. The present sequence is the coding  
CC sequence for one such transcription factor. The transcription factor may  
CC be used to produce a plant having modified gene expression such as a  
CC woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or  
CC mahogany species or to modify the activity of a polypeptide in a plant.  
CC The transcription factors of the present invention are members of the  
CC following families of regulatory proteins: bzip, bzip family of G-box  
CC binding factors, basic helix-loop-helix zipper,  
CC homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2  
CC and EEBFs, zinc finger domains of type 2 Cys2His2, CCAAT box elements  
CC and MYB.  
XX  
50 Sequence 509 BP, 141 A; 147 C; 125 G; 96 T; 0 other;

Query Match	26.0%	Score 261.2	DB 21	Length 509	
Best Local Similarly	77.38%	Pred. No. 3.6e-63			
Matches 317	Conservative	0	Mismatches 93	Indels 0	Gaps 0

[illegible]

RESULT	7
AAC57365	
ID	AAC57365 standard; DNA; 1576 BP
XX	
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AAC57365;	
XX	
DT	25-JAN-2001 (first entry)
XX	



PR 14-JUN-1999; 99US-0139119.  
 PR 16-JUN-1999; 99US-0139452.  
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Best Local Similarity 25.8%; Score 259.8; DB 21; Length 774;

Mismatches 312; Conservative 78.2%; Pred. No. 1.1e-62; Mismatches 87; Indels 0; Gaps 0;

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 Db 1 atggagagatcacatcgtctcgagaaagctcacatgaacaaagagcttgactaaagaa 60



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PR 27-JUL-1999; 99US-0145913.
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PR 02-AUG-1999; 99US-0146386.
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PR 29-OCT-1999; 99US-0162142.

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Query Match 25.2%; Score 253.6; DB 21; Length 639;
Best Local Similarity 78.4%; Pred. No. 5; 2e-61;
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QY 119 gaagatcaacgcctcatcacatcacatccgctgcatggtgaagcgtgcgtccctc 178
DB 61 gaagatcaacgcctcatcacatcacatccgctgcatggtgaagcgtgcgtccctc 120
QY 179 cccaaagctgctggcgtccttagatgtgtaagagtgcaagatgaatgaatgaactac 238
DB 121 cctaatacgtgtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 180
QY 239 ttgagcctgtatcttaagaagaagaatttcactgtgaagaagaatgaatgaatgaatga 298
DB 181 ctgcctcctgacttcaaacgltgaaatttcactgtgtgtgaagaagaatgaatgaatga 240
QY 299 ctccacagcttacttggaaacacacatgctcatgattgctggaagatcaccaagaagaca 358
DB 241 ctccatagttcatttggcaacacacacatgctcatgattgctggaagatcaccaagaagaca 300
QY 359 gataatgagataaagaactacttggaaacacacacatcaacataaagaagcttataagcaga 418
DB 301 gataatgagataaagaactacttggaaacacacacatcaacataaagaagcttataagcaga 360
QY 419 attgaccacaaactcactcgtcctca 446
DB 361 attgaccacaaactcactcgtcctca 388

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RESULT 10
AADD06456 standard; cDNA; 1087 BP.
ID AADD06456;
AC AADD06456;
XX 10-AUG-2001 (first entry)
DT
DE Arabidopsis thaliana transcription factor G664 cDNA.
XX
KW Transcription factor; environmental stress tolerance; gene therapy;
KW plant structure; plant development; ss.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT CDS 104..952
FT /tag= a
FT /product= "Arabidopsis thaliana transcription factor"
XX
XX W0200136598-A1.
XX
XX 25-MAY-2001.
XX
XX 14-NOV-2000; 2000WO-US31458.
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XX 17-NOV-1999; 99US-0166228.
XX
XX 17-APR-2000; 2000US-0197899.
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XX 22-AUG-2000; 2000US-0227439.
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PR 18-JUN-1999; 99US-0139456.
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Query Match 24.6%; Score 247.8; DB 21; Length 1062;  
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    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 274 gaggaagagagagcgtgtgtccttaagctcattgaagtggaagagcgtgcggagattcc 333
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KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
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PN EP1033405-A2.  
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XX 25-FEB-2000; 2000EP-0301439.  
PF 25-FEB-1999; 99US-0121825.  
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PR	26-OCT-1999;	99US-0161359.

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: January 23, 2002, 18:48:37 ; Search time 90.74 Seconds  
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Title: US-09-453-387A-1

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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5	79.2	7.9	3225	1	US-08-306-691B-45
6	79.2	7.9	3225	1	PCT-US93-06251-91
7	79.2	7.9	3230	5	PCT-US93-06251-89
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18	43.2	4.3	282	2	US-08-814-030-2
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24	33	3.3	289	4	US-09-244-796-17
25	33	3.3	2749	4	US-08-344-695-1
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28	31.6	3.1	1215	4	US-08-952-014C-35	Sequence 35, Appl
29	31.6	3.1	7587	4	US-08-378-313-22	Sequence 22, Appl
30	31.6	3.1	48974	4	US-08-920-422-17	Sequence 17, Appl
31	31.4	3.1	2247	4	US-08-760-615-5	Sequence 5, Appl
32	31.2	3.1	2290	6	5312912-1	Patent No. 5312912
33	31	3.1	2217	3	US-08-749-522-5	Sequence 5, Appl
34	31	3.1	3574	4	US-08-467-504-3	Sequence 3, Appl
35	30.8	3.1	344	2	US-08-623-906A-8	Sequence 8, Appl
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42	30.8	3.1	2435	4	US-09-306-593-1	Sequence 1, Appl
43	30.6	3.0	2160	2	US-08-902-853-4	Sequence 4, Appl
44	30.6	3.0	2383	1	US-08-248-466B-13	Sequence 13, Appl
45	30.6	3.0	5336	4	US-09-102-528-11	Sequence 11, Appl

## ALIGNMENTS

RESULT 1  
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; Sequence 1, Application US/08722626B  
; Patent No. 5939601  
; GENERAL INFORMATION:  
; APPLICANT: Yang, Yimong  
; APPLICANT: Kiessig, Daniel, F.  
; TITLE OF INVENTION: NOVEL GENES ASSOCIATED WITH ENHANCED  
; TITLE OF INVENTION: NOVEL GENES ASSOCIATED WITH ENHANCED  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman  
; STREET: 1601 Market Street Suite 720  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103-2307  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/722, 626B  
; FILING DATE: 27-SEP-1996  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pat Hagan  
; REGISTRATION NUMBER: 27,643  
; REFERENCE/DOCKET NUMBER: 97-0010  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215 563-4100  
; TELEFAX: 215 563-4044  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1344 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; FEATURE:  
; NAME/KEY: Coding Sequence

LOCATION: 148...981  
OTHER INFORMATION:  
US-08-722-626B-1

Query Match 16.1%; Score 162.2; DB 2; Length 1344;  
Best Local Similarity 66.4%; Pred. No. 3.5e-39;  
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DB 448 GACATGAATTAATAAATGTTGGCACACCACTTGAGAGAGAGCTCAAA 498

RESULT 2  
US-08-997-251-1  
Sequence 1, Application US/08997251  
Patent No. 6271440  
GENERAL INFORMATION:  
APPLICANT: GUBLER, FRANZ J.  
TITLE OF INVENTION: PLANT REGULATORY PROTEINS III  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESS: Greenlee, Winner and Sullivan, P.C.  
STREET: 5370 Manhattan Boulevard  
CITY: Boulder  
STATE: CO  
COUNTRY: US  
ZIP: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/08/997,251  
FILING DATE: 23-DEC-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO AU96/00383  
FILING DATE: 21-JUN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU PN6470/95  
FILING DATE: 09-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU PN3779/95  
FILING DATE: 23-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Winner, Ellen P.  
REGISTRATION NUMBER: 28,547  
REFERENCE/DOCKET NUMBER: 110-97  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 499-8080  
TELEFAX: (303) 499-8089  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2220 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Hordeum vulgare  
STRAIN: Himalaya  
DEVELOPMENTAL STAGE: Seed  
TISSUE TYPE: Aleurone layer  
IMMEDIATE SOURCE:  
CLONE: HvGAMYB  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 275...1933  
US-08-997-251-1

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Best Local Similarity 59.2%; Pred. No. 3.2e-23;  
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RESULT 3  
US-08-997-251-3  
Sequence 3, Application US/08997251  
Patent No. 6271440  
GENERAL INFORMATION:  
APPLICANT: GUBLER, FRANZ J.  
TITLE OF INVENTION: PLANT REGULATORY PROTEINS III  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESS: Greenlee, Winner and Sullivan, P.C.  
STREET: 5370 Manhattan Boulevard  
CITY: Boulder  
STATE: CO  
COUNTRY: US  
ZIP: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/997,251  
FILING DATE: 23-DEC-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO AU96/00383  
FILING DATE: 21-JUN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU PN6470/95  
FILING DATE: 09-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU PN3779/95  
FILING DATE: 23-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Winner, Ellen P.  
REGISTRATION NUMBER: 28,547  
REFERENCE/DOCKET NUMBER: 110-97  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 499-8080  
TELEFAX: (303) 499-8089  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2352 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
ORIGINAL SOURCE:  
ORGANISM: Oryza sativa  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 396..2054  
US-08-997-251-3

Query Match 10.9%; Score 109.2; DB 4; Length 2352;  
Best Local Similarity 59.8%; Pred. No. 4.3e-23;  
Matches 183; Conservative 0; Mismatches 123; Indels 0; Gaps 0;  
QY 95 aacaaagtgctgagcaaaagagaaagtcaagcgtcatcacatcagcgtgcat 154  
DB 516 AAGAAAGGGGCAATGACGCTCGGCGAGGAGCGCCATCTGTGAGCTAGTGAAGAACAC 575  
QY 155 ggtgaagctgctgagcgtccctcccaagctgctgctgctgctgctgctgct 214  
DB 576 GGGCAGGGGAAGTGAAGCGGCTGCAAGAACACCGGGCTGTCCGGCTCGGGAAGAC 635  
QY 215 tgcagatgaatgaataactactgagcgtgactgaagagagaaattcaactgaa 274  
DB 636 TGCCGCGCTCCGCTGGCGCAACCTGAGGCGCCCAACCTCAAGAGGGGCTTCACCGCC 695  
QY 275 gaagaagtgagctatatactcaagcttcaagcttcaagcttcaagcttcaagct 334  
DB 696 GAGGAGGAGAGCTATCTCCAGCTCCAGCTCCAGATGGGGAACAGTGGCTCGGATG 755  
QY 335 gctgaagattaccagaagaacagataatgagataaagaactctgaacacacacac 394  
DB 756 GCCGCTATTTCGCGAGGGGCGACTGATATGAATAAGATTACTGATCTGATATA 815  
QY 395 aaaga 400  
DB 816 AAGAGA 821

RESULT 4  
PCT-US93-06251-90  
Sequence 90, Application PC/TUS9306251  
GENERAL INFORMATION:  
APPLICANT: Wickstrom, Eric and Rife, Jason P.  
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: NY  
COUNTRY: USA  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/06251  
FILING DATE: 19930630  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Digilio, Frank S.  
REGISTRATION NUMBER: 31,345  
REFERENCE/DOCKET NUMBER: 8586  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 516-742-4343  
TELEFAX: 516-742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 90:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1035 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
PCT-US93-06251-90

Query Match 7.9%; Score 79.2; DB 5; Length 1035;  
Best Local Similarity 54.9%; Pred. No. 3e-14;  
Matches 178; Conservative 0; Mismatches 143; Indels 3; Gaps 1;  
QY 82 aaagctctaccacaagaagtgctgacacaagaagaagtaacgcctcatcaacta 141  
DB 120 AACCCTGAGCTCATCAAGAGTCTCTTGACCAAGAAAGATCAGAGATGATAGACT 179  
QY 142 catcgctgcatagtgtgaagctgtgagcttccctcccaagctctggtgcttag 201  
DB 180 TGTACGAATATGCGTCCGAAACGTTGTCTGTATTCGAACGACCTAAAGGGG--AG 236  
QY 202 agtgtgaagatgtgaagtaagatgaataactactgagctgactcctaagagag 261  
DB 237 AATTGAAATCAATGTAGGAGAGGTGTCATACCATTTGATCCAGACACTTAAGAAAC 296  
QY 262 aaattcaactgaagaagatgagcttcatcaagcttcaagcttcaagcttcaagct 321  
DB 297 CTTCTGAGAGAGAGAGAGAGAGATTTATTACAGACACACAGAGACTGGGGAACAG 356  
QY 322 atgtcatgtattgtctggaagattaccagaagaagacagataatgagataaagaact 381  
DB 357 AGGGGAGAAATCGCAAGCTACTGCTGAGCAGTAATGATTAATCTATCAAGAACACTG 416  
QY 382 gaacacacacatcaaaaagaagct 405  
DB 417 GAATTTACAAATCGTGGAGAGT 440

RESULT 5  
US-08-306-691B-45  
Sequence 45, Application US/08306691B  
Patent No. 5734039  
GENERAL INFORMATION:  
APPLICANT: Calabretta, Bruno  
APPLICANT: Skoraki, Tomasz  
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES  
NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seidel, Gonda, Lavorina & Monaco, P.C.

STREET: Two Penn Center, Suite 1800  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19102

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/306,691B  
FILING DATE: September 15, 1994  
CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Monaco, Daniel A.

REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 8321-8

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8383

TELEFAX: (215) 568-5549

TELEX: NO. 5734039e

INFORMATION FOR SEQ. ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 3225 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-08-306-691B-45

Query Match 7.9%; Score 79.2; DB 1; Length 3225;  
Best Local Similarity 54.9%; Pred. No. 5,6e-14;  
Matches 178; Conservative 0; Mismatches 143; Indels 3; Gaps 1;

QY 82 aaaggtcattacacaaaggtgctgagccaaagaagaagtcacgcctcacaacta 141  
DB 371 AAACCCCTGAGCTCATCAAGGGCTCTTGACCAAGAGATCAGAGTGTAGAGCT 430  
QY 142 catcgggtccatggtgtaaggtcgtggtccctccccaagctgctggtcttag 201  
DB 431 TGTACAGAAATACGTCGCCAAACGTTGCTCTTATTGCCAACACTTAAAGCG--AG 487  
QY 202 atgtgtaagaagttgcagattaagaatgaataactacttgagcctgactttaagaag 261  
DB 488 AATTGGAAGAAACATGTAGAGAGGTGGCATTAACCACTGAATCCAGAAATTAAAGAAC 547  
QY 262 aaattcactgaagaagaatgagctatcatcaagcttcacagcttactcttgaaacaa 321  
DB 548 CTCCTGGACAGAGAGGAGACAGAAATTATTATTCAGAGGACACAGAGACTGGGGAACAG 607  
QY 322 atgtgcatgattgctggaagattaccaggaagaacagataatgataaagaactactg 381  
DB 608 ATGGGACAGAAATCGCAAAAGCTACTGCTTGACGACACTGATTAATCATCAAGAACCACTG 667  
QY 382 gaacacacacatacaaaagaagct 405  
DB 668 GAATTCTACAAATGCGTCGGAAGCT 691

RESULT 6  
PCT-US93-06251-91  
Sequence 91, Application PC/TUS9306251  
GENERAL INFORMATION:  
APPLICANT: Wickstrom, Eric and Rife, Jason P.  
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESS: SCULLY, SCOTT, MURPHY & PRESSER

STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: NY  
COUNTRY: USA  
ZIP: 11530

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/06251  
FILING DATE: 19930630

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Digilio, Frank S.

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 8586

TELECOMMUNICATION INFORMATION:

TELEPHONE: 516-742-4343

TELEFAX: 516-742-4366

INFORMATION FOR SEQ. ID NO: 91:

SEQUENCE CHARACTERISTICS:

LENGTH: 3225 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

PCT-US93-06251-91

Query Match 7.9%; Score 79.2; DB 5; Length 3225;  
Best Local Similarity 54.9%; Pred. No. 5,6e-14;  
Matches 178; Conservative 0; Mismatches 143; Indels 3; Gaps 1;

QY 82 aaaggtcattacacaaaggtgctgagccaaagaagaagtcacgcctcacaacta 141  
DB 371 AAACCCCTGAGCTCATCAAGGGCTCTTGACCAAGAGATCAGAGTGTAGAGCT 430  
QY 142 catcgggtccatggtgtaaggtcgtggtccctccccaagctgctggtcttag 201  
DB 431 TGTACAGAAATACGTCGCCAAACGTTGCTCTTATTGCCAACACTTAAAGGG--AG 487  
QY 202 atgtgtaagaagttgcagattaagaatgaataactacttgagcctgactttaagaag 261  
DB 488 AATTGGAAGAAACATGTAGAGAGGTGGCATTAACCACTGAATCCAGAAATTAAAGAAC 547  
QY 262 aaattcactgaagaagaatgagctatcatcaagcttcacagcttactcttgaaacaa 321  
DB 548 CTCCTGGACAGAGAGGAGACAGAAATTATTATTCAGAGGACACAGAGACTGGGGAACAG 607  
QY 322 atgtgcatgattgctggaagattaccaggaagaacagataatgataaagaactactg 381  
DB 608 ATGGGACAGAAATCGCAAAAGCTACTGCTTGACGACACTGATTAATCATCAAGAACCACTG 667  
QY 382 gaacacacacatacaaaagaagct 405  
DB 668 GAATTCTACAAATGCGTCGGAAGCT 691

RESULT 7  
PCT-US93-06251-89  
Sequence 89, Application PC/TUS9306251  
GENERAL INFORMATION:  
APPLICANT: Wickstrom, Eric and Rife, Jason P.  
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESS: SCULLY, SCOTT, MURPHY & PRESSER  
STREET: 400 Garden City Plaza  
CITY: Garden City









OTHER INFORMATION: /label- SnabI  
FEATURE:  
NAME/KEY: -  
LOCATION: 2634..2639  
OTHER INFORMATION: /label- SnabI  
FEATURE:  
NAME/KEY: -  
LOCATION: 3008..3013  
OTHER INFORMATION: /label- HpaI  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..1077  
OTHER INFORMATION: /label- PC1  
OTHER INFORMATION: /note- "region containing promoter of C1 gene"  
FEATURE:  
NAME/KEY: -  
LOCATION: 1078..2134  
OTHER INFORMATION: /label- C1  
OTHER INFORMATION: /note- "coding region of C1 gene"  
FEATURE:  
NAME/KEY: -  
LOCATION: 2135..2430  
OTHER INFORMATION: /label- 3'C1  
OTHER INFORMATION: /note- "region containing polyadenylation signal"  
OTHER INFORMATION: of C1 gene"  
FEATURE:  
NAME/KEY: -  
LOCATION: 1033..1038  
OTHER INFORMATION: /label- TATA-Box  
FEATURE:  
NAME/KEY: -  
LOCATION: 1061..1062  
OTHER INFORMATION: /label- transcript-init  
OTHER INFORMATION: /note- "transcription initiation site"  
FEATURE:  
NAME/KEY: -  
LOCATION: 1211..1299  
OTHER INFORMATION: /label- 1062  
FEATURE:  
NAME/KEY: -  
LOCATION: 1430..1575  
OTHER INFORMATION: /label- 1430..1575  
FEATURE:  
NAME/KEY: -  
LOCATION: 935..939  
OTHER INFORMATION: /label- C1-S  
OTHER INFORMATION: /note- "TGCAG sequence (in C1 gene) which in the C1-S sequence is changed to TTAGC"  
US-08-485-139-1

Query Match 5.6%; Score 56; DB 2; Length 4059;  
Best Local Similarity 63.2%; Pred. No. 6.1e-07;  
Matches 86; Conservative 0; Mismatches 50; Indels 0; Gaps 0;  
QY 185 gctgctggtctgctagatggtgtaagagtgacagtaagatgataaactctgag 244  
DB 1293 -ggtcagagtttgcgtggtgcgcgacagctgcgcgtcgctgacactacgtccgc 1352  
QY 245 cctgacttaagagaggaatttcctgaagaagaagatgagcttcatcaagcttcac 304  
DB 1353 cccaacatcagagcgccgggcaaacatctcctacgacgagagagatctcatcgcctccac 1412  
QY 305 agttacttgaaaca 320  
DB 1413 AGGCTCCTCGGCACACA 1428

RESULT 14  
US-08-750-357-1  
Sequence 1, Application US/08750357  
Patent No. 6008437  
GENERAL INFORMATION:  
APPLICANT: KREBBERS, ENNO  
APPLICANT: WILLIAMS, MARK

APPLICANT: LEEWANS, Jan  
TITLE OF INVENTION: USE OF ANTHOCYANIN GENES TO MAINTAIN  
TITLE OF INVENTION: MALE STERILE PLANTS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/750,357  
FILING DATE: 21-MAR-1997  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: McGowan, Malcolm K.  
REGISTRATION NUMBER: 39,300  
REFERENCE/DOCKET NUMBER: 018030-100  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4059 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: C1 gene of Zea mays  
FEATURE:  
NAME/KEY: -  
LOCATION: 279..284  
OTHER INFORMATION: /label- HpaI  
FEATURE:  
NAME/KEY: -  
LOCATION: 447..452  
OTHER INFORMATION: /label- EcoRI  
FEATURE:  
NAME/KEY: -  
LOCATION: 1735..1740  
OTHER INFORMATION: /label- AatII  
FEATURE:  
NAME/KEY: -  
LOCATION: 1505..1510  
OTHER INFORMATION: /label- EcoRI  
FEATURE:  
NAME/KEY: -  
LOCATION: 2081..2086  
OTHER INFORMATION: /label- XhoI  
FEATURE:  
NAME/KEY: -  
LOCATION: 2418..2430  
OTHER INFORMATION: /label- SfiI  
FEATURE:  
NAME/KEY: -  
LOCATION: 2669..2674  
OTHER INFORMATION: /label- SnabI  
FEATURE:  
NAME/KEY: -  
LOCATION: 2634..2639  
OTHER INFORMATION: /label- SnabI  
FEATURE:  
NAME/KEY: -  
LOCATION: 3008..3013  
OTHER INFORMATION: /label- HpaI  
FEATURE:

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NAME/KEY: -
LOCATION: 1..1077
OTHER INFORMATION: /label= PCl
OTHER INFORMATION: /note= "region containing promoter of C1 gene"
FEATURE:
NAME/KEY: -
LOCATION: 1078..2134
OTHER INFORMATION: /label= C1
OTHER INFORMATION: /note= "coding region of C1 gene"
FEATURE:
NAME/KEY: -
LOCATION: 2135..2430
OTHER INFORMATION: /label= 3'Cl
OTHER INFORMATION: /note= "region containing polyadenylation signal of C1 gene"
FEATURE:
NAME/KEY: -
LOCATION: 1033..1038
OTHER INFORMATION: /label= TATA-Box
FEATURE:
NAME/KEY: -
LOCATION: 1061..1062
OTHER INFORMATION: /label= transcript-init
OTHER INFORMATION: /note= "transcription initiation site"
FEATURE:
NAME/KEY: -
LOCATION: 1211..1299
FEATURE:
NAME/KEY: -
LOCATION: 1430..1575
FEATURE:
NAME/KEY: -
LOCATION: 935..939
OTHER INFORMATION: /label= CI-S
OTHER INFORMATION: /note= "TGCAG sequence (in CI gene) which in the CI-S sequence"
OTHER INFORMATION: is changed to TTAGG"
US-08-750-357-1

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Query Match 5.6%; Score 56; DB 3; Length 4059;
Best Local Similarity 63.2%; Pred. No. 6.1e-07;
Matches 86; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

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QY 185 gctgctggagctccttaagatggtgtaagattgaagataaactacttgagg 244
DB 1293 GGTGAGGTTTCGTCGGTGGCGCAAGAGCTGCCGCTGCGTGAACCTACCTCCGG 1352
QY 245 cctgacttaagaagaaatttcactgaagaagaagatgagctatcatcaagcttcac 304
DB 1353 CCCAACATCAGCGCGGCAACATCTCTACGAGAGGAGATCTCATCATCTCCGCTCCAC 1412
QY 305 agttacttggaaaca 320
DB 1413 AGGCTCTCGGCACACA 1428

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RESULT 15
US-08-485-139-5
Sequence 5, Application US/08485139
Patent No. 5880331
GENERAL INFORMATION:
APPLICANT: KREBBERS, ENO
APPLICANT: WILLIAMS, MARK
APPLICANT: LEMANS, JAN
TITLE OF INVENTION: USE OF ANTHOCYANIN GENES TO MAINTAIN
TITLE OF INVENTION: MALE STERILE PLANTS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,139
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 010830-096
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4824 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: plasmid pCOL9
FEATURE:
NAME/KEY: -
LOCATION: 396..401
OTHER INFORMATION: /label= EcoRI
FEATURE:
NAME/KEY: -
LOCATION: 2367..2379
OTHER INFORMATION: /label= SfiI
FEATURE:
NAME/KEY: -
LOCATION: 884..888
OTHER INFORMATION: /label= CI-S
OTHER INFORMATION: /note= "TGCAG (in CI) which in CI-S allele is
OTHER INFORMATION: replaced with TTAGG"
US-08-485-139-5

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Query Match 5.6%; Score 56; DB 2; Length 4824;
Best Local Similarity 63.2%; Pred. No. 6.8e-07;
Matches 86; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

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QY 185 gctgctggagctccttaagatggtgtaagattgaagataaactacttgagg 244
DB 1242 GGTGAGGTTTCGTCGGTGGCGCAAGAGCTGCCGCTGCGTGAACCTACCTCCGG 1301
QY 245 cctgacttaagaagaaatttcactgaagaagaagatgagctatcatcaagcttcac 304
DB 1302 CCCAACATCAGCGCGGCAACATCTCTACGAGAGGAGATCTCATCATCTCCGCTCCAC 1361
QY 305 agttacttggaaaca 320
DB 1362 AGGCTCTCGGCACACA 1377

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Search completed: January 23, 2002, 20:22:30
Job time: 5633 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 23, 2002, 18:40:17 ; Search time 1542.92 Seconds  
(without alignments)  
7006.360 Million cell updates/sec

Title: US-09-453-387A-1  
Perfect score: 1006  
Sequence: 1 taacacgcttattcttc.....aatgcttaattataaaaa 1006

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues  
Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

EST:\*  
1: em\_estfun:\*  
2: em\_esthm:\*  
3: em\_estlin:\*  
4: em\_estlpl:\*  
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7: em\_estlpl:\*  
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9: em\_estlpl:\*  
10: gb\_estl:\*  
11: gb\_estl:\*  
12: gb\_hic:\*  
13: gb\_gss:\*  
14: em\_gss\_fun:\*  
15: em\_gss\_hum:\*  
16: em\_gss\_inv:\*  
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18: em\_gss\_pro:\*  
19: em\_gss\_tod:\*  
20: em\_gss\_vit:\*  
21: em\_gss\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	361	35.9	927	11	BG445164 GA_EB002
3	295.8	29.4	757	11	BG889982 EST513633
4	288.6	28.7	526	11	BE801303 sr12d04.y
5	287.4	28.6	526	10	A1771837 EST252937
6	283	28.1	447	10	A1486301 EST244622
7	278	27.6	536	10	BE124666 EST393701
8	275	27.3	549	11	BE802821 sr45a11.y
9	261.4	26.0	603	10	A1731905 BNLGH1112
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18	235	23.4	457	10	AU082322
19	235	23.4	467	10	AU082325
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24	233	23.1	683	10	BE052585
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26	231.2	23.0	425	10	AU408163
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28	226.2	22.5	704	11	B1421740
29	225.8	22.4	446	10	AU184006
30	225.4	22.4	445	10	AU173093
31	220.6	21.9	385	11	BE804943
32	219.6	21.8	564	11	BE611947
33	219.6	21.8	572	10	AM737657
34	219.2	21.8	579	10	A1727146
35	219.2	21.8	620	10	AM011253
36	218.4	21.7	578	10	A1730649
37	217.6	21.6	617	10	BG301049
38	217.6	21.6	624	11	BG301022
39	217.2	21.6	625	11	AM064634
40	216.6	21.5	626	11	BE519041
41	214.8	21.4	656	11	T42000
42	213.4	21.2	473	11	BE627287
43	207.2	20.6	756	11	AU183276
44	205.6	20.4	451	10	BE361115
45	201.6	20.0	590	10	BE361115

#### ALIGNMENTS

RESULT 1  
BF269948 857 bp mRNA EST 07-MAR-2001  
GA\_EB0006B13f Gossypium arboreum 7-10 dpa fiber library Gossypium  
arboreum CDNA clone GA\_EB0006B13f, mRNA sequence.

ACCESSION  
BF269948  
BF269948.1 GI:11200943

KEYWORDS  
SOURCE  
ORGANISM  
Gossypium arboreum.

REFERENCE  
Wing, R.A., Frisch, D., Yu, Y., Malm, D., Rambo, T., Simmons, J., Henry  
'D', Wood, T.C., Leslie, A. and Wilkins, T.A.  
An integrated analysis of the genetics, development, and evolution  
of the cotton fiber  
Unpublished (2000)  
Contact: Wing RA

JOURNAL  
COMMENT  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rwing@clemson.edu

FEATURES  
source  
Seq primer: TAATACGACGCTACGATAGG  
High quality sequence start: 4  
High quality sequence stop: 633.  
Location/Qualifiers  
1..857  
/organism="Gossypium arboreum"  
/strain="AKA"  
/cultur="8400"  
/db\_xref="taxon:29729"









RESULT	7				
BE124666					
LOCUS	BE124666	536 bp	mRNA	EST	07-SEP-2000
DEFINITION	ES393701	GVN	Medicago truncatula	cdna	clone pGVN-67A6, mRNA
ACCESSION	BE124666				

QY	119	gaagatacaagcgtataactaacatccgtygcattcgtgtaaggctgcgtccctc	178
Db	27	ATGGCAGATCTCCTGTTGTGTGAGAAAGCAGCACAAACAAAGTGCTTGGACAAAAAA	86
QY	59	atggagagctacccctctgtctgtcgaaaaggtccataaccacaaggtctcgtgaccacaag	110
Db	147	CCAAAAGCGTGGCGTTGCTTAAGATGTGGCAGAGTTCGAATGAAATGATTAATAC	206
QY	179	cccaaacgtctctggtctgtctagatgtgtgtaagagttcgacagattaagaatgataactac	238
Db	87	GAGAGTGAACGTCCTCATTTACTACATCAACAGCTTCATGTGGGAAAGTTGTTGAGAGTCTCT	146
QY	239	ttagagccctgattcttaagagagagaattcactcaggaagaagaatgagcttatcatcaag	298
Db	207	CTAAGACCTGATCTCAAGAGAGGAACCTCAGCAACGAAGAAATGATCTTATCATTAAC	266
QY	239	cttcacagtttactcttggaacaacaaatgctcatctgattgcttggaagattaccaggaagaaca	358

Db 267 CTCACACCTACTTGGAACAATGCTCTTAATAGCTAGATTACCAGAGACCA 326

Qy 359 gataatgataaagaactactggaacacacacatcaaaagaagcttataagcagagga 418  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 327 GATATGATGATCAACAAATTTACTGGAACACTCATCAACGGAAGAACTCTACAGCGTGA 386

Qy 419 atgatccacaacactcgtctcctcaatcaaacgagccataccaacagtcagcc 478  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 387 GTCGACCTCAACACATCGCTGACTTAAAGACTCAACGATCAACACCATCAATATCCA 446

Qy 479 cc 480

Db 447 CC 448

RESULT 8

BE802821 549 bp mRNA EST 21-NOV-2000

LOCUS srt45a11.y1 Gm-cl051 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl051-981.5, similar to TR:P81395 P81395 MYB-RELATED PROTEIN 330.1, mRNA sequence.

DEFINITION BE802821 GI:10233933

ACCESSION BE802821

VERSION BE802821.1

KEYWORDS soybean, Glycine max

SOURCE Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

ORGANISM 1 (bases 1 to 549)

REFERENCE Shoemaker, R., Kelm, P., Vodkin, L., Erpelidg, J., Coryell, V., Khanna, A., Bolle, B., Maritz, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, J., Peterson, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritters, E., Kohn, S., Shih, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.

TITLE Public Soybean EST Project

JOURNAL Unpublished (1999)

COMMENT Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or info@genomesystems.com web site: www.genomesystems.com  
Insert length: 1111 Std Error: 0.00  
High quality sequence stop: 471.

FEATURES

Source

Location/Qualifiers

1. 549

/organism="Glycine max"

/db\_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-cl051-981"

/clone\_lib="Gm-cl051"

/tissue\_type="floral meristematic mRNA"

/lab\_host="DH10B"

/note="Vector: pBluescript II SK<sup>+</sup> Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from floral meristematic mRNA provided by Dr. Halina Knap of Clemson University. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

BASE COUNT 186 a 142 c 108 g 113 t

ORIGIN

Query Match 27.3%; Score 275; DB 11; Length 549;  
Best Local Similarity 78.9%; Pred. No. 2.3e-49;  
Matches 340; Conservative 0; Mismatches 90; Indels 1; Gaps 1;

Qy 54 aactatgtagaagatacctctgtgtgtaaaagcttaccacaagaagtcgctgacaa 113  
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Db 35 AATCCATGGAGATGCCCTGTGTGCGAGAAAGACACACCAACAAAGAGCTTGACCA 94

Qy 114 aagagaagatacaacgctcctcatcaatcacatccgtgcacatgtaaggtcgtgcyt 173  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 95 AAGAGAAACAGACGAGCCCTCATCACTACATCAAGCTCCATGCGTAAGCGCTTGAGAT 154

Qy 174 cccctcccaaaagctgctggtgctcttagatgtagtgaagagttgcaagattcaagatgataa 233  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 155 CCTCCCAAGCTGCTGCGCTTCTCAGATGTGCGCAAGAGTTGACAGACTCAGATGATTA 214

Qy 234 actacttgagcgctgatttaagagaggaattcactgaagaagaatgaagcttaca 293  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 215 ATTACTCAGACCTGATC-TCAGAGAGGCACTTCACTGAAGAGAGAGATGACTCATCA 273

Qy 294 tcaagctcacagtttactcttggaacacaatggtcatgtatgctgtaagattaccaggaa 353  
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Db 274 TAACTCCTATAGCTTACTTCTGGAACAATGCTTTTGATAGCTGCAAGTTACTGTGAA 333

Qy 354 gaacagataatgataaagaactactggaacacacacatcaaaagaagcttataagca 413  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 334 GAACCGATACGAAATATTAATATGGAACACTCACTCAATCAAGAAAGAACTCTACAC 393

Qy 414 gaggatgatccacaacactcgtctcctcaatcaaacgagccataccaacagatca 473  
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Db 394 GCGGATCAACCTCTGACTCATCTGCTCACTCAACGCTGCTCCGCCCTCGGCAACCA 453

Qy 474 cagcccccacc 484

Db 454 CCGTCACAGCC 464

RESULT 9

A1731905 603 bp mRNA EST 11-JUN-1999

LOCUS BNLGH11247 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to myb protein 308 - garden snapperdragon, mRNA sequence.

DEFINITION A1731905

ACCESSION A1731905

VERSION A1731905.1

KEYWORDS EST.

SOURCE upland cotton.

ORGANISM Gossypium hirsutum

REFERENCE Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

AUTHORS Blewitt, M., Matz, E.C., Davy, D.F. and Burr, B.

TITLE ESTs from developing cotton fiber

JOURNAL Unpublished (1999)

COMMENT Contact: Ben Burr  
Biology Department  
Brookhaven National Laboratory  
Upton, NY 11973, USA  
Tel: 516-344-3396  
Fax: 516-344-3407  
Email: burrb@bnl.bnl.gov  
Seq primer: T3 primer.

FEATURES

Source

Location/Qualifiers

1. 603

/organism="Gossypium hirsutum"

/cultivar="Acala Maxxa"

/db\_xref="taxon:3635"

/clone\_lib="Six-day Cotton fiber"

/tissue\_type="immature fiber"



## COMMENT

Contact: Deborah A. Samac  
Department of Plant Pathology  
University of Minnesota  
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA  
Tel: 612 625 1243  
Fax: 651 649 5058  
Email: debbyapuccini.crl@umn.edu  
Minnesota sequence name: M2592206  
TIGR sequence name: MTFJ0821K  
More information is available at:  
<http://chryslr.tamu.edu/medicago>  
Seq. primer: SKmod (CTA GAA CTA gta gat cc).  
Location/Qualifiers

## FEATURES

## SOURCE

1. 730  
/organism="Medicago truncatula"  
/cultivar="genotype A17"  
/db\_xref="taxon:3880"  
/clone="pDSIL-3M20"  
/tissue\_lib="DSIL"  
/tissue\_type="Leaves infected with Colletotrichum trifolii"  
/dev\_stage="cotyledons and primary leaves harvested 5 and 8 days after inoculation with Colletotrichum trifolii"  
/lab\_host="E. coli strain XLOLR"  
/note="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2: XhoI; cDNA was prepared from polyA+ enriched RNA from cotyledons and primary leaves harvested 5 and 8 days after inoculation with Colletotrichum trifolii. The cDNA was directionally ligated into the uni-ZAP XR vector from StrataGene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Aassist helper phage and propagated in XLOLR cells. Note: EST may be of fungal origin."  
BASE COUNT 278 a 140 c 119 g 193 t  
ORIGIN

Query Match 25.5%; Score 256.8; DB 10; Length 730;  
Best Local Similarity 75.0%; Pred. No. 1.8e-45;

Matches 321; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 42 attgatttgaactgtaggaagcattcctgtgtgaaaggtcattaccacaag 101  
DB 90 AGTACTTAATCAAAATATGGAGATGATCCTTGTGAAAGCTCATACAAACAAG 149  
QY 102 gtgcctggaagaagaagaatacaagcctcattcaactcaactcgtgtccatgtgaag 161  
DB 150 GAGCTTGACAAAAGAAAGATGATGATATATATATATAGGCACATGCTGAAG 209  
QY 162 gctgtcgttccctcccaagctgtggtccttagatgtgtgaaaggtcattaccacaag 221  
DB 210 GTTGTGAGATCTCTCCCTTAAGCAGCTGCTTACTCCGATGTGTTAAAGTTGCTGC 269  
QY 222 taagatgataaactactgagcctgaacttaagaagaagaattcactgaagaagaag 281  
DB 270 TCCGGTGGATTAATCACTCAGCCAGACTTAACGTGATGTTTACAGAAAGAAAG 329  
QY 282 atgagcttaccatcaagcttcagttactgtgaaacaagaatggtcattgattgtgaa 341  
DB 330 ATTAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 389  
QY 342 gattacagaagaagaagaatagataagaagaactactgagacacacacacacacacac 401  
DB 390 GATTACAGAGAAGAGATATAGATTAAGATTAATTTGGACACTCATATTAAGAGAA 449  
QY 402 agcttataagcagaagaatgataccacaactcctgcctctcattcaacaagccacata 461  
DB 450 AGCTTTGAATGAGGATGACCTCTCTACTATAGGCTTTAAAGAAAGTTTTCATT 509  
QY 462 caaacaca 469  
DB 510 CTCATATCA 517

## RESULT 12

## BF716393

## LOCUS

## DEFINITION

BF716393 603 bp mRNA EST 02-JAN-2001  
saal19f01.y1 Gm-c1058 glycine max cDNA clone GENOME SYSTEMS CLONE  
ID: Gm-c1058-1801.5' similar to SW:MYB3\_MALIZE P20025 MYB-RELATED  
PROTEIN ZM38. // mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

soybean.  
Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.  
1 (bases 1 to 603)  
Shoemaker, R., Kelm, P., Vodkin, L., Expelting, J., Corryell, V., Khanna,  
A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,  
Wyllie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers,  
Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk,  
R., Rittler, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann,  
R., Waterston, R. and Wilson, R.  
Public Soybean EST Project  
Unpublished (1999)  
Contact: Shoemaker R./Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estewatson.wustl.edu

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

This clone is available through: Genome Systems, Inc. 4633 World  
Parkway Circle St. Louis, Missouri 63134 For further information  
call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)  
427-3324 or contact: clones@genomesystems.com or  
info@genomesystems.com web site: www.genomesystems.com  
High quality sequence stop: 413.  
Location/Qualifiers

## FEATURES

## SOURCE

1. 603  
/organism="Glycine max"  
/db\_xref="taxon:3847"  
/clone="GENOME SYSTEMS CLONE ID: Gm-c1058-1801"  
/tissue\_lib="Gm-c1058"  
/tissue\_type="Hypocotyl, 2 week old seedlings, etiolated"  
/lab\_host="DH10B"  
/note="Vector: pBluescript II SK-; Site\_1: EcoRI; Site\_2:  
XhoI; The cDNA library was constructed from mRNA isolated  
from hypocotyl tissue of 2 week old etiolated seedlings  
for P1468916. Complementary DNA was synthesized from mRNA  
using a primer consisting of a poly(dT) sequence with a  
XhoI restriction site. EcoRI adapters were ligated to the  
blunt-ended cDNA fragments followed by XhoI digestion. The  
cDNA fragments were directionally cloned into the  
EcoRI-XhoI restriction site of the pBluescript vector. The  
ligated cDNA fragments were transformed into DH10B host  
cells (Gibco BRL). This library was constructed in the  
laboratory of Dr. Randy Shoemaker at Iowa state  
university."

## BASE COUNT

## ORIGIN

189 a 149 c 133 g 132 t  
Query Match 25.4%; Score 255.4; DB 11; Length 603;  
Best Local Similarity 74.4%; Pred. No. 3.8e-45;  
Matches 322; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 52 gtaactgattggaagcattcctgtgtgaaaggtcattaccacaagaaggtcgtgac 111  
DB 36 GTTAAGTATGGAGGCTCCCTCTGTAAGAAAGCTCACACAAAGAGTGCATGAC 95  
QY 112 caagaggaagaagaagaagcctcattcaactcattcgtgtccatggtgaaggtcgtgac 171

LOCUS	DEFINITION	LOCUS	DEFINITION
AI897672	AI897672 580 bp	AI897672	AI897672 580 bp
EST267115	EST267115 tomato ovary, TAU Lycopersicon esculentum cDNA clone	EST267115	EST267115 tomato ovary, TAU Lycopersicon esculentum cDNA clone
CLD30E23	CLD30E23, mRNA sequence.	CLD30E23	CLD30E23, mRNA sequence.

ACCESSION	A1897012
VERSION	A1897672.1
KEYWORDS	GI:5603574
SOURCE	EST.
ORGANISM	tomato.
	Lycopersicon esculentum

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 580)				
Alcala, J., Vredalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E.				
Liang, F., Upton, J., Ronling, C.M., Craven, M.B., Fujii, C.Y., Bowman,				
C.L., Nierman, W., Fraser, C.M., Venter, J.C., Martin, G.B., Tankley				
, S.D. and Giovannoni, J.				
Generation of ESTs from tomato carpel tissue				
Unpublished (1999)				
Contact: CGGI				

**SOURCE**

Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>  
5 prime sequence.

**FEATURES**

Location/Qualifiers  
1..360

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/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="CLEDD30E23"
/clone_1bp="tomato ovary, TAMU"
/tissue_type="carpel"
/dev_stage="5 days pre-anthesis to 5 days post-anthesis"
/lab_host="XL1-Blue MRF"
/note="Vector: p Bluescript SK(-); site_1: EcoRI; site_2:
XhoI; CLED - Tomato Carpel EST Library. OligoDT'-primed and
directionally cloned cDNA in vector Lambda ZAP II with 5'
and 3' ends located at the EcoRI and XhoI sites,
respectively."

```

OY	59	atggagacatcaccttctgttgtgtaaaagctctataccacaagaagtgcctggaaccaaaagg	118
Db	92	ATGGGAAGGTCACTGTGTGTGAGAAGGACATACAAACAAGAGCATGAGCTAAAGAA	151
OY	119	gaagatcaacgcctcatcaaacatcacccgtgtgtccatgyltgaagctgtgtgccttcctc	178
Db	152	GAAGATGAAGAAGCTAATTCTTCACTTAGAGCTCAATGCGAAGGTGTGTGGAGGTCCTCT	211
OY	179	cccaagctgtctggcgtcgtctatgtagtgtgtaagagtgtagattaaagatgataaacac	238
Db	212	CCTAAGCTGTGCGACTTCTTCGATGCGGCTAAAGTTGTGCTCGAAGGATTAATATTAC	271
OY	239	ttgagcctgtatcttaagaagagaatattcatattgaagaagaagatgagtttccatcaag	298
Db	272	TTAAACCTGACCTTTAAACGTGTGTAACCTTACTGGAAGAAGAGTCACTCATTAACAA	331
OY	299	cttcacagtttacttggaaacaagaatggtcatattgtcttgggaagattaccagaagaaca	358
Db	332	CTCCATAGCCTCTTTGGAACAAGTGTGCTTAATAGCAGGAAGATTACCAAGAAACACA	391
OY	359	gataatgagataaagaacactctggaacacacacatcaaaagaagaagcttaataagaagga	418
Db	392	GATAACGAGATTAATAAATCTATTGGAAACACATATTAAGCGAAAGCTCTTGAGTCGAGGT	451
OY	419	attgtatccacaacatcatcgtcctctccaatcaaaacgycgaataccaacaacagltcaagc	477
Db	452	ATTGATCCACACACACATGATTCATTCATGTGCTCCTACACTCAATACCAAAAGTTACAAAC	510

RESULT	14
LOCUS	AL373528
DEFINITION	MTBB01D01F1 MtBB Medicago truncatula cDNA clone MCB01D01 T3, mRNA
	468 bp mRNA EST 03-AUG-2000

ACCESSION	sequence.
AL373528	
KEYWORDS	AL373528.1 GI:9673280
SOURCE	EST.
ORGANISM	barrel medic. Medicago truncatula Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae Medicago.
REFERENCE	1 (bases 1 to 468)
AUTHORS	Journé,E.P., Crespeau,H., van-Tuinen,D., Guzy,J., Jallion O., Kubicki,R., Kuhn,M., Lecomte,C., Lottin,F., Mouton R., Parnis A.,

TITLE	JOURNAL	COMMENT
<p>Niebel, A., Carreau, V., Chagnatier, O., Kaim, P., Gianfranceschi, P., V. and Gamas, P.</p> <p>Medicago truncatula ESTs from Simorghizobium meliloti-induced root nodules</p> <p>unpublished (2000)</p> <p>Contact: Genoscope</p> <p>Genoscope - Centre National de Sequencage</p> <p>Bp 191 91006 EVRY cedex - France</p> <p>Email: seque@genoscope.cns.fr Web : www.genoscope.cns.fr</p> <p>Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de Biologie Moléculaire des Relations Plantes-Microorganismes, CNRS-INRA, Bp 27 31326 Castanet-Tolosan Cedex, France (Email : Mt-est@toulouse.inra.fr Website : <a href="http://sequence.toulouse.inra.fr/Mtruncatula.html">http://sequence.toulouse.inra.fr/Mtruncatula.html</a>).</p> <p>Location/Qualifiers</p> <p>1. 468</p>		

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/organism="Medicago truncatula"
/cultivar="Jemalong"
/db_xref="taxon:3880"
/clone="MtBB01D01"
/clone_1b="MtRB"
/tissue_type="symbiotic root nodules"
/dev_stage="harvested 4 days post inoculation with

```

COMMENT

CONTACT: DIXON RA

Search completed: January 23, 2002, 19:54:04  
Job time: 4427 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2002, 20:20:42 ; Search time 67.35 Seconds  
(Without alignments) 323.349 Million cell updates/sec

Title: US-09-453-387A-2  
1584  
Sequence: 1 MGRSPCEKATNKGAWKRE.....RNCQNSNGEYCYCRPLDS 294

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1567.5	99.0	293	22 AAB82481	Cotton transcript
2	768	48.5	257	21 AAG30441	Arabidopsis thalia
3	762	48.1	236	21 AAG08529	Arabidopsis thalia
4	762	48.1	236	21 AAG49909	Arabidopsis thalia
5	762	48.1	236	22 AAB67842	Amino acid sequenc
6	728.5	46.0	255	21 AAB33306	Pinus radiata tran
7	723	45.6	282	21 AAG32956	Arabidopsis thalia
8	723	45.6	282	22 AAE02476	Arabidopsis thalia
9	702	44.3	246	21 AAG30442	Arabidopsis thalia
10	701	44.3	225	21 AAB33322	Pinus radiata tran
11	684	43.2	274	21 AAG31297	Arabidopsis thalia

12	684	43.2	274	22 AAE02485	Arabidopsis thalia
13	681.5	43.0	269	21 AAG29948	Arabidopsis thalia
14	681.5	43.0	269	22 AAE02486	Arabidopsis thalia
15	681.5	43.0	278	21 AAG29947	Arabidopsis thalia
16	676.5	42.7	144	21 AAB33305	Pinus radiata tran
17	674.5	42.6	212	21 AAG33153	Arabidopsis thalia
18	665.5	42.0	226	21 AAB33301	Pinus radiata tran
19	650	41.0	125	21 AAG32927	Zea mays protein f
20	650	41.0	145	21 AAG32926	Eucalyptus grandis
21	646	40.8	171	21 AAB33246	Cotton transcript
22	626.5	39.6	226	22 AAB82482	Arabidopsis thalia
23	620.5	39.2	238	21 AAG29949	Arabidopsis thalia
24	608.5	38.4	201	21 AAG33154	Arabidopsis thalia
25	604	38.1	139	21 AAB33036	Pinus radiata tran
26	595	37.6	122	21 AAG21226	Zea mays protein f
27	584.5	36.9	153	21 AAB33239	Eucalyptus grandis
28	565	35.7	107	21 AAB33201	Pinus radiata tran
29	565	35.7	107	21 AAB33289	Pinus radiata tran
30	564	35.6	107	21 AAB33275	Pinus radiata tran
31	562	35.5	391	21 AAB33304	Pinus radiata tran
32	555.5	35.1	412	21 AAB33303	Pinus radiata tran
33	554.5	35.0	345	21 AAG34523	Arabidopsis thalia
34	553.5	34.9	176	21 AAB33283	Pinus radiata tran
35	548	34.6	266	21 AAG22138	Arabidopsis thalia
36	543	34.3	414	21 AAG29245	Arabidopsis thalia
37	541	34.2	266	22 AAE01890	Pinus radiata tran
38	539.5	34.1	119	21 AAB33033	Arabidopsis thalia
39	539.5	34.1	350	21 AAG46107	Arabidopsis thalia
40	539.5	34.1	362	22 AAE01937	Eucalyptus grandis
41	536	33.8	192	21 AAB33255	Arabidopsis thalia
42	534.5	33.7	324	22 AAE01923	Pinus radiata tran
43	533.5	33.7	148	21 AAB33044	Pinus radiata tran
44	533	33.6	109	21 AAB33186	Eucalyptus grandis
45					

## ALIGNMENTS

RESULT 1  
ID AAB82481 standard; Protein: 293 AA.  
XX AAB82481;  
AC  
XX 22-AUG-2001 (first entry)  
DT  
XX Cotton transcription factor GhMYB 1.  
DE  
XX  
KW GhMYB 1; MYB; cotton; transcription factor; transgenic plant.  
XX  
OS Gossypium hirsutum cv. Acala SU-2.  
XX  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 44..45  
FT has a Gly residue between residues 44  
FT and 45 of the present sequence  
FT  
FT  
XX  
XX  
XX MO200140250-A1.  
XX  
XX PD  
XX 07-JUN-2001.  
XX  
XX 01-DEC-2000; 2000MO-US32731.  
XX  
XX 02-DEC-1999; 99US-0453387.  
XX  
XX (REGC) UNTV CALIFORNIA.  
XX  
XX Wilkins TA;  
XX  
XX WPI; 2001-397938/42.  
XX  
XX N-PSDB; AAF90594.  
XX  
XX



Modulating transcription in plants for improving cotton fiber quality,  
comprises introducing a recombinant expression cassette comprising a  
promoter operably linked to a sequence encoding a MYB polypeptide -  
Claim 5; Page 41; 50pp; English.

The present sequence is that of cotton MYB transcription factor  
GhMYB 1. The protein includes a highly conserved N-terminal  
DNA-binding domain, and a non-conserved C-terminal transcriptional  
regulatory domain. It also contains a Cys-rich domain similar to a  
zinc finger motif. The sequence was deduced from GhMYB 1 cDNA  
isolated from a Gossypium hirsutum cv. Acala 5J-2 3-day pre-anthesis  
ovule cDNA library. GhMYB 1 transcripts are relatively abundant and  
appear to be expressed in all tissues examined. A claimed method  
of modulating transcription in a plant involves introducing into  
the plant a recombinant expression cassette comprising a promoter  
operably linked to a heterologous polynucleotide encoding a MYB  
protein, especially GhMYB 1 or GhMYB 6. The plant is especially a  
cotton plant, and the promoter directs expression of the  
polynucleotide in cotton fibres or roots. Valuable phenotypes  
can be conferred on the plant by this method, e.g. increased fibre  
quality, alteration of root architecture, and enhanced growth.  
The GhMYB 1 gene is particularly useful for increasing levels of  
gene expression in plant fibres to increase fibre yield, length,  
strength and fineness.

Sequence 293 AA:

Query Match 99.0%; Score 1567.5; DB 22; Length 293;  
Best Local Similarity 99.7%; Pred. No. 5.2e-141;  
Matches 293; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

1 MGRSPCEKAHNTKGAATMEEDRLNIVYHVGCGKRSLEPKAGLRCGSCRIKWINY 60  
1 MGRSPCEKAHNTKGAATMEEDRLNIVYHVGCGKRSLEPKAGLRCGSCRIKWINY 59  
61 LRPDLKRCNTEEDDELILKLSLGNKMSLNGRLPGRTNEIKNWNTHIRKILRSRG 120  
60 LRPDLKRCNTEEDDELILKLSLGNKMSLNGRLPGRTNEIKNWNTHIRKILRSRG 119  
121 IDPQTHRLPNTANTNTVTAPELDFRNSPTSVSKSSSIKNSLDFNNEQFKNSTDSL 180  
120 IDPQTHRLPNTANTNTVTAPELDFRNSPTSVSKSSSIKNSLDFNNEQFKNSTDSL 179  
181 EEPNCASSGMMTDEEOQELHKKOQYGPENGDINIELSGIYSADSSRSNNASASK 240  
180 EEPNCASSGMMTDEEOQELHKKOQYGPENGDINIELSGIYSADSSRSNNASASK 239  
241 PAVDNNPQFLQAOAVAKAVCLCMQLGFTSEICRNCNSNSNGFYSCRPDLS 294  
240 PAVDNNPQFLQAOAVAKAVCLCMQLGFTSEICRNCNSNSNGFYSCRPDLS 293

RESULT 2

AAG30441  
ID AAG30441 standard: Protein; 257 AA.

AC AAG30441;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 36393.

KM Protein identification; signal transduction pathway; metabolic pathway;  
hybridisation assay; genetic mapping; gene expression control; promoter;  
termination sequence.

OS Arabidopsis thaliana.

PM EPI033405-A2.

XX

PD 06-SEP-2000.  
XX 25-FEB-2000; 2000EP-0301439.  
XX 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
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 PR 28-OCT-1999; 99US-0161920.  
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Query Match

Best Local Similarity 48.54; Score 768; DB 21; Length 257;  
 Matches 160; Conservativity 55.68; Pred. No. 5.9e-65; Mismatches 53; Indels 42; Gaps 7;

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 Db 1 mgsrpscekahnmkgatkeedqllvdyirkhgecsmslpaaalqrcgkscrlrwmy 60  
 QY 61 LRPLDKRGNTFEEDDELLIKLSLGNKWSLIAGRLPERTDNEINYNWTHIKRLISRG 120  
 Db 61 lrpldkrgntfeedeelliklsllgnkwsliagrlpdrtdneiknywthikrlisrg 120  
 QY 121 IDPQTHRPLNQTANTNTVATTELDFRNSPTSVSSSSIKNSLDFNNEPQKSTDSL 180  
 Db 121 idpqrhrlpntantntvtatleldfrnsptsvssssiknsldfnnepqkstdsl 180  
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 Db 181 eep-----nctassgmtdeeqlelkkqoyspngodinelelsig-ivsadsr-vsn 233  
 QY 234 ANSAESKPKYDNNNFQLEQAMVAKAVCLQWLGFTSEICRNCONSN 281  
 Db 234 ansaeskrpydnnnfqleqamvakavclqwlgtseicrnconsn 281  
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RESULT 3  
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 ID AAG08529 standard; Protein; 236 AA.  
 AC AAG08529;  
 XX  
 DT 17-OCT-2000 (first entry)  
 XX Arabidopsis thaliana protein fragment SEQ ID NO: 6103.

XX Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter  
 KW termination sequence.

*Arabidopsis thaliana*.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

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PR 31-AUG-1999; 99US-0151438.
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PR 13-SEP-1999; 99US-0153758.
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PR 20-SEP-1999; 99US-0154779.
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PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
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PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
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PR 22-OCT-1999; 99US-0160980.
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Query Match 48.1%; Score 762; DB 21; Length 236;

Best Local Similarity 58.9%; Pred. No. 1.9e-64; Indels 22; Gaps 5;

Matches 145; Conservative 39; Mismatches 40; Indels 22; Gaps 5;

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QY 1 MGRSPCEKAKHNTKNGKAMTEEDDRLINIRVHGEGCWRSLPKAAGLLRCGKSCRLRWINY 60
DB 1 mgrspcecahntkngkamtteeddrlydrtrnhgsgcwrslpkasgllrcgscrlrwiny 60
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DB 61 lrpdlkrgntfeddelilklslgnkwsliagrlpgrdneikntwnthikrlisrg 120
QY 121 IDPQTHRPANQANTMT-VTAPFELDPFRNSPTYSKSSSTINPDLDFVYNEFOFNSNDS 179
DB 121 idpqtthrpnanqantmt-vtapfelldpfrnsptyskssstinpdlfdvynefofnsnds 179
QY 180 LEEPNTASSGNTDEEOQLKHKOOKYGPSNGQ-DINLELSIGVIGVSDSRVSNANSAE 238
DB 180 leepntassgntdeeoqlkhhkookygpsngq-dinlelsigvlgvsgdsrvsnansae 238
QY 239 SKPKVD 244
DB 239 skpkvd 244
QY 221 skpvd 226
DB 221 skpvd 226

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RESULT 4
ID AAG49909
AC AAG49909;
DT 18-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63188.
KW Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
XX EP1033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-0301439.
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127462.
XX 06-APR-1999; 99US-0128234.
XX 08-APR-1999; 99US-0128714.
XX 16-APR-1999; 99US-0129845.
XX 19-APR-1999; 99US-0130077.
XX 21-APR-1999; 99US-0130449.
XX 23-APR-1999; 99US-0130510.
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XX 05-MAY-1999; 99US-0132484.
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PR 08-OCT-1999; 99US-0158232.  
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PR 29-OCT-1999; 99US-0162142.

## Query Match

48.1%; Score 762; DB 21; Length 236;

Best Local Similarity 58.9%; Pred. NO. 1.9e-64; Mismatches 40; Indels 22; Gaps 5;

Matches 145; Conservative 39; Mismatches 40; Indels 22; Gaps 5;

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DB 1 mgrspcekahntkngawtkeedgrlvdyirnhsgcwrslpkasgllrcgksclrlwiny 60  
OY 61 LRPDLKRGNTFEDEDEILILHSILGNKKSILARLUGRTNEIKNYNTIHKRLILRS 120  
DB 61 lrpdlkrgnftdedeqlllhlshlgnkksilagrllpgrtneiknyntihkrlilshg 120  
OY 121 IDPOTHRPLNOTANTNT-VTAPTELDPRNSPTSVSKSSSIKNPSUDFVYNBFOFSNTDS 179  
DB 121 idpqrhnglneaktsvsgvvp-----lqndaveysfsmavkpkten 163

QY 180 LEEPNCTASSGNTDEEOQLHKQOYGPSNGO-DINLELSIGIVSADSSRVSNANSAE 238  
 Db 164 ssd-ngastsgttddedlrg-ngecydsdngshklnldltlfgswsgrlvgyssad 220  
 QY 239 SKPKVD 244  
 Db 221 skpwc 226

RESULT 5  
 AAB67842  
 ID AAB67842 standard; Protein: 236 AA.  
 XX AAB67842;  
 XX 29-JUN-2001 (first entry)  
 DE Amino acid sequence of a plant transcription factor G208.  
 XX Transcription factor; flowering time; transgenic plant; vernalisation;  
 KM plant development; plant physiology; flowering.  
 XX Arabidopsis thaliana.  
 OS WO200126459-A2.  
 PN 19-APR-2001.  
 PD 11-OCT-2000; 2000WO-US28141.  
 PF 12-OCT-1999; 99US-0159464.  
 PR 08-NOV-1999; 99US-0164132.  
 PR 17-NOV-1999; 99US-0166228.  
 PR 17-APR-2000; 2000US-0197899.  
 PR 22-AUG-2000; 2000US-0227439.

PA (MEND-) MENDEL BIOTECHNOLOGY INC.  
 PA (RATC/) RATCLIFFE O.  
 PA (HEAR/) HEARD J.  
 PA (SAMA/) SAMAHA R.  
 PA (CREE/) CREELMAN R.  
 PA (KEDD/) KEDDIE J.  
 PA (JIANG/) JIANG C.  
 PA (REUB/) REUBER L.  
 PA (RIEC/) RIECHMANN J. L.  
 XX Ratcliffe O, Heard J, Samaha R, Creelman R, Keddie J, Jiang C;  
 PI Reuber L, Riechmann JL;  
 XX WPI: 2001-266398/27.  
 DR N-PSDB; AAF80412.

PT New transgenic plant comprises a recombinant polynucleotide encoding a  
 PT plant transcription factor polypeptide and has a modified flowering  
 PT time or vernalization requirement -  
 XX Example 7; Page 105-106; 108pp; English.

XX The present sequence represents a plant transcription factor protein  
 CC which modifies the flowering time of a plant. The polynucleotide  
 CC sequence is used to produce transgenic plants which have a modified  
 CC flowering time or a modified vernalisation requirement. The  
 CC polynucleotides and polypeptides are useful for modifying plant  
 CC development, physiology or biochemistry such that the modified plants  
 CC have a trait advantage over wild type plants. In particular they are  
 CC useful for accelerating, delaying or preventing flowering. The  
 CC polynucleotides are also useful as nucleic acid probes and primers.  
 CC They may be used to identify proteins that can modify the activity of  
 CC the transcription factor.  
 XX Sequence 236 AA:

Query Match. 48.1%; Score 762; DB 22; Length 236;  
 Best Local Similarity 58.9%; Pred. No. 1.9e-64;  
 Matches 145; Conservative 39; Mismatches 40; Indels 22; Gaps 5;

QY 1 MGRSPCCERAKHTKNGATKKEEDQRLIVYRHGGCRSLPKAAGLRCGSCRRRTNY 60  
 Db 1 mgrspccerakhtkngatkeedqrlivdyrhnbgcwrslpksagllrcgscrrlwnly 60  
 QY 61 LRPDLKRGNTFEEDDELIILKHSILGNKWSLIAGRLPQRTDNEIKNYNTIKRKLIERG 120  
 Db 61 lrpdlkrgntfededqllkhsilgnkwsliagrlpqrtneiknyntikrkliershg 120  
 QY 121 IDPOTHRPLINOTANTNT-VTAPTELDPFRNSPTSVSKSSIKNPISLDFVNEFOKNTDS 179  
 Db 121 idpqtlnrqnesktsqvvp-----lqndaveyfsfnlavpkten 163  
 QY 180 LEEPNCTASSGNTDEEOQLHKQOYGPSNGO-DINLELSIGIVSADSSRVSNANSAE 238  
 Db 164 ssd-ngastsgttddedlrg-ngecydsdngshklnldltlfgswsgrlvgyssad 220  
 QY 239 SKPKVD 244  
 Db 221 skpwc 226

RESULT 6  
 AAB33306  
 ID AAB33306 standard; Protein: 255 AA.  
 XX AAB33306;  
 XX 25-JAN-2001 (first entry)  
 DE Pinus radiata transcription factor protein sequence #346.  
 XX Pinus radiata transcription factor; gene expression; eucalyptus; pine; acacia;  
 KM poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor;  
 KM basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;  
 KM homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain;  
 XX type 2 Cys2His2; CCAT box element; MYB.  
 OS Pinus radiata.  
 PN WO200053724-A2.  
 PD 14-SEP-2000.  
 PF 09-MAR-2000; 2000WO-US06112.  
 PR 11-MAR-1999; 99US-0266513.  
 PR 18-AUG-1999; 99US-0149485.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 XX Wood M, McGrath A, Shenk MA, Glenn M;  
 PI Wood M, McGrath A, Shenk MA, Glenn M;  
 XX WPI: 2000-579369/54.  
 DR New isolated polynucleotide encoding a plant transcription factor for  
 PT producing a plant e.g. a woody plant, preferably eucalyptus or pine,  
 PT having modified gene expression or modified activity of a polypeptide  
 PT

Claim 8: Pages 717-718; 747pp; English.  
 XX The present invention relates to novel plant transcription factors from  
 CC Eucalyptus grandis or Pinus radiata. The present sequence is one such  
 CC transcription factor. The transcription factor may be used to produce a  
 CC plant having modified gene expression such as a woody plant e.g. a  
 CC eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or  
 CC to modify the activity of a polypeptide in a plant. The transcription  
 CC factors of the present invention are members from the following families

CC of regulatory proteins: bzip, bzip family of G-box binding factors, basic  
CC helix-loop-helix zipper, homeobox/homeodomain/homeobox/MADS, homeodomain  
CC zipper, LIM domain, AP2 and EREBS, zinc finger domains of type 2  
CC Cys2His2, COAT box elements and MYB.

XX Sequence 255 AA;

Query Match 46.0%; Score 728.5; DB 21; Length 255;  
Best Local Similarity 51.7%; Pred. No. 3.4e-61;  
Matches 155; Conservative 32; Mismatches 52; Indels 61; Gaps 10;

QY 1 MGRSPCEKATNTNGAMTKEDDRIINIRVHGECMRSIPKAGLLRGKSGRLWVINY 60  
DB 1 MGRSPCEKATNTNGAMTKEDDRIINIRVHGECMRSIPKAGLLRGKSGRLWVINY 60  
QY 61 LRPDLKGNFTFEDEDELIKRLHSLGNKMSLAGRLPGRTDNEIKRYWNTTHIKRLISRG 120  
DB 61 LRPDLKGNFTFEDEDELIKRLHSLGNKMSLAGRLPGRTDNEIKRYWNTTHIKRLISRG 120  
QY 121 IDPQTHRPPLNQTANTNTVTAPT-----ELDFRNSPTSVSKSSIKNPGL-DFVNEPQF 173  
DB 121 IDPQTHRPPLNQTANTNTVTAPT-----ELDFRNSPTSVSKSSIKNPGL-DFVNEPQF 173  
QY 174 KSNMDSLEPRKCTASSGNTTDEEOQOLHKKQVGPSPNGODINLEISIGIVSADSSRVSN 233  
DB 174 KSNMDSLEPRKCTASSGNTTDEEOQOLHKKQVGPSPNGODINLEISIGIVSADSSRVSN 233  
QY 167 ERESSESPMEP-----ATKDEEH-----PDINLIDICLIPVHSPATSR 206  
DB 167 ERESSESPMEP-----ATKDEEH-----PDINLIDICLIPVHSPATSR 206  
QY 234 ANS-----AESKPKYDNNNFOLFQAMVAKAVCLCQOLGFTSEICNCONSNS--NGEYVS 287  
DB 207 ASVVDGVLDAKPN-----SVSCHMGLQVNYGVCENYCEASAGVSFYT 252

RESULT 7

ID AAG32956 standard; Protein: 282 AA.

AC AAG32956;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 39857.

KW Protein identification; signal transduction pathway; metabolic pathway;

KM hybridisation assay; genetic mapping; gene expression control; promoter;

XX termination sequence.

OS Arabidopsis thaliana.

XX EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 25-MAR-1999; 99US-0126264.

XX 29-MAR-1999; 99US-0126785.

XX 01-APR-1999; 99US-0127462.

XX 06-APR-1999; 99US-0128234.

XX 08-APR-1999; 99US-0128714.

XX 16-APR-1999; 99US-0129845.

XX 19-APR-1999; 99US-0130077.

XX 21-APR-1999; 99US-0130449.

XX 23-APR-1999; 99US-0130510.

XX 23-APR-1999; 99US-0130891.

XX 28-APR-1999; 99US-0131449.

XX 30-APR-1999; 99US-0132048.

XX 30-APR-1999; 99US-0132407.

XX 04-MAY-1999; 99US-0132484.

PR 05-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

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 QY 73 EDELLIKLHSLGNKWSLIRGRLPGRTDNEIKYWTHTIRKILSRIDQTHRPLNOT 132  
 DB 62 eedelliklshslgnkwsrpragjqrqgkacrlmmylrpdkrgntfe 120  
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 DB 121 -----svpspslqndvvelthldfsqvpkpepreetlgnvnc-e 160  
 QY 188 SSGMTDEECOEOLARKKOQYSPNGODINELSIG-IVSADSSR-VSNVANSAESKPKYDN 245  
 DB 161 ssgtsek-----ygnedwvlnlelsvqpyryestrtkvavdsaestrwgs 210  
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Query Match	44.3%	Score 701	DB 21	Length 225
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Db	1	mgrrspceekantnkawckgeddrliantirahgeggwslpkaaallrcgkscrlrwny	60	
Oy	61	LRPDIKGNFTFEEDELIKLHSLGKMSLGIARLPRTDNEIKNYNWTIKRLLISG	120	
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	PR	21-JUL-1999;	99US-0144684.	PR	18-OCT-1999;	99US-0159638.
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	PR	22-JUL-1999;	99US-0145087.	PR	21-OCT-1999;	99US-0160770.
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 QY 61 LRPDLKRGNTFEDEDELLIKHSLGNKWSLIAGRLPGFTDNEIKMYWNTIHKRLISRG 120  
 Db 61 lrpdlkrgntfeedeallikhsllgnkwsliatrlpgftdneikmywntihvkrkllrk 120  
 QY 121 IDPQTHRPPLNQTANTNTATPELDFRNSPTSVSKSSSIKNSLDNPNYNEFOKSNDSL 180  
 Db 121 ldpqthrpplnektsg-----dsdsdktedply-----kllsfqpl 158  
 QY 181 EEPNCTASSGWTDEEOQLHKKQYGPNSNG--DINLELSIGIVSADSSRVSNANSAE 238  
 Db 159 ek---lanfg-----derlqkrveyveercldlnlelrlspwpqdklh----- 200  
 QY 239 SKPKVDNNNFQLEQAMVAKAVCLQWLGFTGTSICRNCON-----SNSNGFYS 287  
 Db 201 -----dernlrlfgr---vkysacsrfgfngkcc-scnnvkcgtedsssssys 245

RESULT 12  
 AAE02485  
 ID AAE02485 standard; Protein: 274 AA.  
 AC AAE02485;  
 DT 10-AUG-2001 (first entry)  
 DE Arabidopsis thaliana transcription factor G664 homologue, G197.  
 KW Transcription factor; environmental stress tolerance; gene therapy;  
 KM plant structure; plant development.  
 OS Arabidopsis thaliana.  
 PH Key Location/Qualifiers  
 FT Domain 14..119  
 XX /note="Conserved domain"  
 PN MO200136598-A1.  
 PD 25-MAY-2001.  
 XX 14-NOV-2000; 2000MO-US31458.  
 PF 17-NOV-1999; 99US-0166238.  
 PR 17-APR-2000; 2000US-0197899.  
 PR 22-AUG-2000; 2000US-0227439.  
 XX (MEND-) MENDEL BIOTECHNOLOGY INC.  
 PA (PINE/) PINEDA O.  
 PA (YUGC/) YU G.  
 PA (CREE/) CREELMAN R.  
 PA (RIEC/) RIECHMANN J L.  
 PA (HEAR/) HEARD J.  
 PA (RATC/) RATCLIFFE O.  
 PA (REUB/) REUBER L.  
 PA (KEDD/) KEDDIE J.  
 XX Pineda O, Yu G, Creelman R, Riechmann JL, Heard J, Ratcliffe O,  
 PI Reuber L, Keddie J;  
 DR MPI: 2001-336000/35.  
 DR N-PSDB; AAD06465.  
 XX Nucleic acids encoding plant transcription factor polypeptides, useful  
 PT for altering the environmental stress tolerance characteristics of  
 PT plants -  
 PS Claim 4; Page 101-102; 116pp; English.  
 CC The present amino acid sequence is Arabidopsis thaliana  
 CC transcription factor homologue. This novel transcription factor  
 CC is useful for modifying a plant's phenotype in desirable ways, such as

CC modifying a plants environmental stress. The transcription factor is  
 CC encoded by environmental stress tolerance gene derived from  
 CC Arabidopsis thaliana. The transcription factors and the genes encoding  
 CC them are used to alter the structure and developmental characteristics  
 CC of plants such as soybean, wheat, corn, potato, cotton, rice, oilseed  
 CC rape, sunflower, alfalfa, sugarcane, turf, banana, blackberry, papaya,  
 CC strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, onion,  
 CC cucumber, eggplant, grapes, honey dew, lettuce, mango, melon, blueberry,  
 CC peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato,  
 CC watermelon, roseaceous fruits and/or vegetable brassicas. These sequences  
 CC are also used for modifying traits associated with environmental stresses  
 CC tolerance, such as freezing, chilling, heat, drought, water saturation,  
 CC salt, photooxidations, radiation and ozone. The transcription factors  
 CC are used in gene therapy.  
 SO Sequence 274 AA.

Query Match 43.2%; Score 684; DB 22; Length 274;  
 Best Local Similarity 49.5%; Pred. No. 6, 5e-57;  
 Matches 146; Conservative 30; Mismatches 61; Indels 58; Gaps 9;

QY 1 MGSPCCCKAHNTKNGAWTEEDORLNIYRVHGGCWRSLPKAGLRCGKSCRLRWINY 60  
 Db 1 mgspccckhntkngawteedkklisylkahgegcwrsiprsaglgcgscrlrwiny 60  
 QY 61 LRPDLKRGNTFEDEDELLIKHSLGNKWSLIAGRLPGFTDNEIKMYWNTIHKRLISRG 120  
 Db 61 lrpdlkrgntfeedeallikhsllgnkwsliatrlpgftdneikmywntihvkrkllrk 120  
 QY 121 IDPQTHRPPLNQTANTNTATPELDFRNSPTSVSKSSSIKNSLDNPNYNEFOKSNDSL 180  
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 Db 159 ek---lanfg-----derlqkrveyveercldlnlelrlspwpqdklh----- 200  
 QY 239 SKPKVDNNNFQLEQAMVAKAVCLQWLGFTGTSICRNCON-----SNSNGFYS 287  
 Db 201 -----dernlrlfgr---vkysacsrfgfngkcc-scnnvkcgtedsssssys 245

RESULT 13  
 AAG29948  
 ID AAG29948 standard; Protein: 269 AA.  
 AC AAG29948;  
 DT 17-OCT-2000 (first entry)  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 35717.  
 KW Protein identification; signal transduction pathway; metabolic pathway;  
 KM hybridisation assay; genetic mapping; gene expression control; promoter;  
 OS Arabidopsis thaliana.  
 XX Arabidopsis thaliana.  
 XX EP1033405-A2.  
 PD 06-SEP-2000.  
 PD 25-FEB-2000; 2000EP-0301439.  
 PF 25-FEB-1999; 99US-0121825.  
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 PR 29-MAR-1999; 99US-0126785.  
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 PR 06-APR-1999; 99US-0128234.

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ID AAG29947 standard; Protein; 278 AA.  
XX AAG29947;  
AC  
XX  
DT 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35716.  
XX  
XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
OS Arabidopsis thaliana.  
XX  
XX EP1033405-A2.  
XX  
XX PD 06-SEP-2000.  
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XX PF 25-FEB-2000; 2000EP-0301439.  
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PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 43.0%; Score 681.5; DB 21; Length 278;  
Best Local Similarity 48.8%; Pred. No. 1.2e-56;  
Matches 142; Conservative 35; Mismatches 59; Indels 55; Gaps 8;

QY 1 MGRSPCEKATNTNGATWKEEDQRLINTIRVHGEQWRLPRKAGLLRQCKSGLRWINY 60  
DB 10 mgrpcekekmnkgawckederlvayikngcgwtslpraagllrcgksclrlwiny 69  
QY 61 LRPLKRGNFEEDEELIKLSLGNKWSLTAGRLPGRTDNEIKNYWTHIKRKLISRG 120  
DB 70 lrplkrgnfnchdeliklsllgnkwsllaarlpgrtdeiknywthikrkliskg 129  
QY 121 IDPOTHRPLNOTANTNTVATPELDFRNSPTSVSKSSSIKNPSLDNFYNFQFKSNTDSL 180

DB 130 ldpnthrginea-----kisdllkttdqivkdsfvkfee---tdksqd 171  
QY 181 EEPNCTASSGTTDEQ---QEQLHKQOYGPSNGODINLEISIGIVSADSSRVSNANSA 237  
DB 172 qkqmkylrnglsvckeervveeki-----gpdlnlelrlsppwqgreistctas 221  
QY 238 ESKPKVDNNNQFLQAMVAKAVCLCMQDGFSTSEICRCNQNNSNGFYX 208  
DB 222 rfy-----ymendnec-----ssetvk-cqtensssl-sy 248

Search completed: January 23, 2002, 21:11:32  
Job time: 3050 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2002, 20:22:32 ; Search time 64.93 seconds  
(without alignments)  
101.894 Million cell updates/sec

Title: US-09-453-387A-2  
Perfect score: 1584  
Sequence: 1 MGRSPCCCKATNKGMATKE.....RNCONSNNGFYSCRPIDS 294

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	493	31.1	278	2	US-08-722-626B-2
2	394.5	24.9	553	4	US-08-997-251-4
3	393.5	24.8	553	4	US-08-997-251-2
4	283.5	17.8	156	4	US-08-928-941D-4
5	283.5	17.8	156	4	US-08-928-941D-36
6	283.5	17.8	156	4	US-09-280-590A-4
7	282.5	17.8	156	4	US-09-280-590A-46
8	167	10.5	51	1	US-08-519-103-17
9	167	10.5	51	1	US-09-018-635-17
10	163	10.3	51	1	US-08-519-103-16
11	163	10.3	51	1	US-08-519-103-16
12	163	10.3	51	4	US-09-018-635-16
13	163	10.3	51	4	US-09-018-635-19
14	160	10.1	51	1	US-08-519-103-18
15	160	10.1	51	4	US-09-018-635-18
16	137	8.6	802	4	US-08-928-941D-29
17	136.5	8.6	760	4	US-09-280-590A-29
18	136.5	8.6	760	4	US-09-280-590A-29
19	132.5	8.4	94	2	US-08-814-030-1
20	127	8.0	761	4	US-08-928-941D-1
21	127	8.0	761	4	US-09-280-590A-1
22	123.5	7.7	372	4	US-08-928-941D-16
23	123.5	7.7	372	4	US-09-280-590A-16
24	121.5	7.7	52	1	US-08-519-103-13
25	121.5	7.7	52	1	US-08-519-103-14
26	121.5	7.7	52	4	US-09-018-635-13
27	121.5	7.7	52	4	US-09-018-635-14

28	117.5	7.4	50	4	US-09-156-316-4	Sequence 4, Appl
29	116.5	7.4	50	4	US-09-156-316-5	Sequence 5, Appl
30	116.5	7.4	50	4	US-09-156-316-6	Sequence 6, Appl
31	112.5	7.1	169	4	US-08-928-941D-35	Sequence 35, Appl
32	112.5	7.1	169	4	US-09-280-590A-45	Sequence 45, Appl
33	101	6.4	711	3	US-08-613-009A-21	Sequence 21, Appl
34	92	5.8	412	2	US-08-741-134-2	Sequence 22, Appl
35	90.5	5.7	1202	1	US-08-425-061-22	Sequence 22, Appl
36	90.5	5.7	1202	2	US-08-825-886-22	Sequence 23, Appl
37	90.5	5.7	1363	1	US-08-425-061-23	Sequence 23, Appl
38	90.5	5.7	1363	2	US-08-825-886-23	Sequence 24, Appl
39	90.5	5.7	1852	1	US-08-425-061-24	Sequence 24, Appl
40	90.5	5.7	1852	2	US-08-825-886-24	Sequence 25, Appl
41	90.5	5.7	1863	1	US-08-425-061-16	Sequence 16, Appl
42	90.5	5.7	1863	1	US-08-598-591-2	Sequence 2, Appl
43	90.5	5.7	1863	1	US-08-480-784-2	Sequence 2, Appl
44	90.5	5.7	1863	1	US-08-483-553-2	Sequence 2, Appl
45	90.5	5.7	1863	2	US-08-603-753D-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-08-722-626B-2  
Sequence 2, Application US/08722626B  
Patent No. 5939601  
GENERAL INFORMATION:  
APPLICANT: Yang, Yinnong  
INVENTOR: Klessig, Daniel, F.  
TITLE OF INVENTION: NOVEL GENES ASSOCIATED WITH ENHANCED  
DISEASE RESISTANCE IN PLANTS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dann, Dorfman, Herrell and Skillman  
STREET: 1601 Market Street Suite 720  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103-2307  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTED Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/722,626B  
FILING DATE: 27-SEP-1996  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pat Hagan  
REGISTRATION NUMBER: 27,643  
REFERENCE/DOCKET NUMBER: 97-0010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215 563-4100  
TELEFAX: 215 563-4044  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 278 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
ORIGINAL SOURCE:  
US-08-722-626B-2

Query Match 31.1%; Score 493; DB 2; Length 278;  
Best Local Similarity 38.8%; Pred. No. 5.5e-44;  
Matches 111; Conservative 40; Mismatches 75; Indels 60; Gaps 7;

QY 1 MGRSPCKAHTNKGAWTEEDQRLINIRVHGEGRSLPKAAGLRGKSCRLRWINY 60  
DB 1 MVRAPCCCKMGKAGKPMWEEDQILISFIQTNGHWRALPKAAGLRGKSCRLRWINY 60  
QY 61 LRPDLKRGFTFEEDDLIKLSLGNKSLINGRLPGRDNEKNWNTNHIKRLISRG 120  
DB 61 LRPDLKRGFTFEEDDLIKLSLGNKSLINGRLPGRDNEKNWNTNHIKRLISRG 118  
QY 121 IDPQHRPLNGANTNTVAPTELDPRNSP--TSVSKSSIKNPSLDENEFQKSNSTD 178  
DB 119 YKPPONSKRHSKSKNDKSGFTTSSNSDITINQKHIDSVLPN----- 167  
QY 179 SLEPNCRTASSGAT---DEEQEQLHKKQOYGPNSGODINLELSIGIVSADSSRVNA 234  
DB 168 ---SPOISSTEMSTYTLVDHDMVYI--KQEV-----M 196  
QY 235 NSAESKPKVD-----NNNEQLEQAMAKAVCLCWLQGFCT 270  
DB 197 ESSEYFPEIDESEFMTDELFTDNNMSSSTDHYVAVANQELQVQLPPSS 242

RESULT 2  
US-08-997-251-4  
; Sequence 4, Application US/08997251  
; Patent No. 6271440

GENERAL INFORMATION:  
APPLICANT: GUBLER, FRANZ J.  
APPLICANT: JACOBSEN, JOHN V.  
TITLE OF INVENTION: PLANT REGULATORY PROTEINS III  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
STREET: 5370 Manhattan Boulevard  
CITY: Boulder  
STATE: CO  
COUNTRY: US  
ZIP: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/997,251  
FILING DATE: 23-DEC-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO AU96/00383  
FILING DATE: 21-JUN-1996  
APPLICATION NUMBER: AU PN6470/95  
FILING DATE: 09-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU PN3779/95  
FILING DATE: 23-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Winner, Ellen P.  
REGISTRATION NUMBER: 28,547  
REFERENCE/DOCKET NUMBER: 110-97  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 499-8080  
TELEFAX: (303) 499-8089  
INFORMATION FOR SEQ. ID NO. 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 553 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-997-251-4

Query Match 24.9%; Score 394.5; DB 4; Length 553;  
Best Local Similarity 35.4%; Pred. No. 4.2e-33;  
Matches 107; Conservative 49; Mismatches 91; Indels 55; Gaps 13;

QY 14 KGAMTEEDQRLINIRVHGEGRSLPKAAGLRGKSCRLRWINYLRPDLKRGFTFE 73  
DB 42 KGPWTSADPAIDLVDYVKKHGEGRNNAVQKNTGLFRCGKSCRLRWNTNHIKRLISRG 101  
QY 74 EDLLIKLSLGNKSLINGRLPGRDNEKNWNTNHIKRLISRGIDPQHRPLNOTA 133  
DB 102 EERLLIQLHSMKMGKMAHAHLPGRDNEKNWNTNHIKRLISRGIDPQHRPLNOTA 160  
QY 134 NRTVYAPTELDP---RNSPTSVSKSSIKNPSLDENEFQKSNSTDLE-EPNCTASS 189  
DB 161 NEDQOCS---DFDQGENLSNDLNLNGLYLP--DFTCD--NFANSEALPYAPHLSAVS 213  
QY 190 ---GWTDEEQEQLHKKQOYGPNSGODINLELSIGIVSADSSRVNSANSAESKPKVD 244  
DB 214 ISNLLGSEFASKSCSEFMDVQVQTG-----NLKQSDGVLPGLSDPTINGVIS----VD 261  
QY 245 ---NNNEQLEQAMAKAVCLCWLQGF-----GTSET-----CRNCONSNGFTSYC 289  
DB 262 QFSNDSKELKQA-----VGFDYLHENSSTSKITAPPGALNGSHAFLNGFSAS 310  
QY 290 RP 291  
DB 311 RP 312

RESULT 3  
US-08-997-251-2  
; Sequence 2, Application US/08997251  
; Patent No. 6271440

GENERAL INFORMATION:  
APPLICANT: GUBLER, FRANZ J.  
APPLICANT: JACOBSEN, JOHN V.  
TITLE OF INVENTION: PLANT REGULATORY PROTEINS III  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
STREET: 5370 Manhattan Boulevard  
CITY: Boulder  
STATE: CO  
COUNTRY: US  
ZIP: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/997,251  
FILING DATE: 23-DEC-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO AU96/00383  
FILING DATE: 21-JUN-1996  
APPLICATION NUMBER: AU PN6470/95  
FILING DATE: 09-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU PN3779/95  
FILING DATE: 23-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Winner, Ellen P.  
REGISTRATION NUMBER: 28,547  
REFERENCE/DOCKET NUMBER: 110-97  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 499-8080  
TELEFAX: (303) 499-8089

Query Match	17.8%	Score 282.5	DB 4	Length 156
Best Local Similarity	51.0%	Pred. No. 4e-22		
Matches 53, Conservative		20, Mismatches 28,	Indels 3,	Gaps 2;

OY 14 KGAWTKEDORLINTYRVHGEQWRSLEPK-AAGLRQCGKSCRLRWNTYLRPDLKRGNETE 72  
DB 55 KGPWTKEDORVLTVOYKIGPKRMSVYAKHLKG--RIGKQCRERHNNHNLNPEVKKTSWTE 112  
OY 73 EDEDLIKLHSLGNKMSLIAGRLPGRTDNEIKNYWNTHIKRL 116  
DB 113 EEDRIIYQAHKRIGNRMAEIAKLPLPGRTDNLKNNHNSYMRKRV 156

RESULT 6  
US-09-280-590A-4  
Sequence 4, Application US/09280590A  
Patent No. 6303772  
GENERAL INFORMATION:  
APPLICANT: Hirai, Hiroshi  
Sheri, Charles  
Inoue, Kazushi  
Bodner, Sarah M.  
TITLE OF INVENTION: CYCLIN-D BINDING FACTOR, AND USES THEREOF  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David A. Jackson, Esq.  
STREET: 411 Hackensack Ave, Continental Plaza, 4th Floor  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/280,590A  
FILING DATE: 29-Mar-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 1340-1-002 N CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-487-5800  
TELEFAX: 201-343-1684  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Mus musculus  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-280-590A-4

Query Match 17.8%; Score 282.5; DB 4; Length 156;  
Best Local Similarity 51.0%; Pred. No. 4e-22; Indels 3; Gaps 2;  
Matches 53; Conservative 20; Mismatches 28;

OY 14 KGAWTKEDORLINTYRVHGEQWRSLEPK-AAGLRQCGKSCRLRWNTYLRPDLKRGNETE 72  
DB 55 KGPWTKEDORVLTVOYKIGPKRMSVYAKHLKG--RIGKQCRERHNNHNLNPEVKKTSWTE 112  
OY 73 EDEDLIKLHSLGNKMSLIAGRLPGRTDNEIKNYWNTHIKRL 116  
DB 113 EEDRIIYQAHKRIGNRMAEIAKLPLPGRTDNLKNNHNSYMRKRV 156

RESULT 7  
US-09-280-590A-46  
Sequence 46, Application US/09280590A  
Patent No. 6303772  
GENERAL INFORMATION:  
APPLICANT: Hirai, Hiroshi  
Sheri, Charles  
Inoue, Kazushi  
Bodner, Sarah M.  
TITLE OF INVENTION: CYCLIN-D BINDING FACTOR, AND USES THEREOF  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David A. Jackson, Esq.  
STREET: 411 Hackensack Ave, Continental Plaza, 4th Floor  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/280,590A  
FILING DATE: 29-Mar-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 1340-1-002 N CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-487-5800  
TELEFAX: 201-343-1684  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: YES  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
ORGANISM: Gallus gallus  
SEQUENCE DESCRIPTION: SEQ ID NO: 46:  
US-09-280-590A-46

Query Match 17.8%; Score 282.5; DB 4; Length 156;  
Best Local Similarity 51.0%; Pred. No. 4e-22; Indels 3; Gaps 2;  
Matches 53; Conservative 20; Mismatches 28;

OY 14 KGAWTKEDORLINTYRVHGEQWRSLEPK-AAGLRQCGKSCRLRWNTYLRPDLKRGNETE 72  
DB 55 KGPWTKEDORVLTVOYKIGPKRMSVYAKHLKG--RIGKQCRERHNNHNLNPEVKKTSWTE 112  
OY 73 EDEDLIKLHSLGNKMSLIAGRLPGRTDNEIKNYWNTHIKRL 116  
DB 113 EEDRIIYQAHKRIGNRMAEIAKLPLPGRTDNLKNNHNSYMRKRV 156

RESULT 8  
US-08-519-103-17  
Sequence 17, Application US/08519103  
Patent No. 5733730  
GENERAL INFORMATION:  
APPLICANT: delange, Tilla  
TITLE OF INVENTION: TELOMERE REPEAT BINDING FACTOR AND  
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USE THEREOF

NUMBER OF SEQUENCES: 21  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: KLAUBER & JACKSON  
 STREET: 411 Hackensack Avenue  
 CITY: Hackensack  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07601  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/519,103  
 FILING DATE: 25-AUG-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Crane-Feury, Sharon E.  
 REGISTRATION NUMBER: 36,113  
 REFERENCE/DOCKET NUMBER: 600-1-142  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-487-5800  
 TELEFAX: 201-343-1684  
 TELEX: 133521  
 INFORMATION FOR SEQ ID NO: 17:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 51 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-519-103-17

Query Match 10.5%; Score 167; DB 1; Length 51;  
 Best Local Similarity 56.9%; Pred. No. 1,1e-10;  
 Matches 29; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

OY 65 LKRGNTEDEDELLIKLSLGNKWSLIGRLPGRTDNEIKYNWTHIRK 115  
 Db 1 VKKSCWTEEDRITCEAHKVLGNRAEIAKMLPGRTDNVKNHNMSTIKRK 51

RESULT 9  
 US-09-018-635-17  
 Sequence 17, Application US/09018635  
 Patent No. 6297356  
 GENERAL INFORMATION:  
 APPLICANT: de Lange, Titia  
 APPLICANT: Broccoli, Dominique  
 APPLICANT: Smogorzewska, Agata  
 TITLE OF INVENTION: TELOMERE REPEAT BINDING FACTOR AND  
 TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USE THEREOF  
 NUMBER OF SEQUENCES: 52  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: KLAUBER & JACKSON  
 STREET: 411 Hackensack Avenue  
 CITY: Hackensack  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07601  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/018,635  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: David A. Jackson

REGISTRATION NUMBER: 26,742  
 REFERENCE/DOCKET NUMBER: 600-1-142 CIP1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-487-5800  
 TELEFAX: 201-343-1684  
 TELEX: 133521  
 INFORMATION FOR SEQ ID NO: 17:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 51 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-018-635-17

Query Match 10.5%; Score 167; DB 4; Length 51;  
 Best Local Similarity 56.9%; Pred. No. 1,1e-10;  
 Matches 29; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

OY 65 LKRGNTEDEDELLIKLSLGNKWSLIGRLPGRTDNEIKYNWTHIRK 115  
 Db 1 VKKSCWTEEDRITCEAHKVLGNRAEIAKMLPGRTDNVKNHNMSTIKRK 51

RESULT 10  
 US-08-519-103-16  
 Sequence 16, Application US/08519103  
 Patent No. 5733730  
 GENERAL INFORMATION:  
 APPLICANT: deLange, Titia  
 TITLE OF INVENTION: TELOMERE REPEAT BINDING FACTOR AND  
 TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USE THEREOF  
 NUMBER OF SEQUENCES: 21  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: KLAUBER & JACKSON  
 STREET: 411 Hackensack Avenue  
 CITY: Hackensack  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07601  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/519,103  
 FILING DATE: 25-AUG-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Crane-Feury, Sharon E.  
 REGISTRATION NUMBER: 36,113  
 REFERENCE/DOCKET NUMBER: 600-1-142  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-487-5800  
 TELEFAX: 201-343-1684  
 TELEX: 133521  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 51 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-519-103-16

Query Match 10.3%; Score 163; DB 1; Length 51;  
 Best Local Similarity 54.9%; Pred. No. 3e-10;  
 Matches 28; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

OY 65 LKRGNTEDEDELLIKLSLGNKWSLIGRLPGRTDNEIKYNWTHIRK 115

Db 1 VKKSWTEEDRIIYEAHKLGNRMALIAKLPGRTDINSIKHNWSTMRK 51

RESULT 11  
US-08-519-103-19  
Sequence 19, Application US/08519103  
Patent No. 5733730

## GENERAL INFORMATION:

APPLICANT: delange, Titia  
TITLE OF INVENTION: TELOMERE REPEAT BINDING FACTOR AND  
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USE THEREOF  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: KLAUBER & JACKSON  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/519,103  
FILING DATE: 25-AUG-1995

## CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Crane-Feury, Sharon E.  
REGISTRATION NUMBER: 36,113  
REFERENCE/DOCKET NUMBER: 600-1-142  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-487-5800  
TELEFAX: 201-343-1684  
TELEX: 133521

## INFORMATION FOR SEQ. ID NO: 19:

SEQUENCE CHARACTERISTICS:  
LENGTH: 51 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-519-103-19

Query Match 10.3%; Score 163; DB 1; Length 51;  
Best Local Similarity 56.9%; Pred. No. 3e-10;  
Matches 29; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

Qy 65 LKRGNTFEEDRLIKLSLGNKWSLIGRLPGRTDNEIKNWNTHIRK 115

Db 1 IKKTATKEDELIYQALHELGNOMAKIAKRLPGRTDIAIKHNWSTMRK 51

RESULT 12  
US-09-018-635-16  
Sequence 16, Application US/09018635  
Patent No. 6297356

## GENERAL INFORMATION:

APPLICANT: de Lange, Titia  
APPLICANT: Broccoli, Dominique  
APPLICANT: Smogorzewska, Agata  
TITLE OF INVENTION: TELOMERE REPEAT BINDING FACTOR AND  
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USE THEREOF  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: KLAUBER & JACKSON  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA

ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/018,635  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: David A. Jackson  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-142 CIP1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-487-5800  
TELEFAX: 201-343-1684  
TELEX: 133521  
INFORMATION FOR SEQ. ID NO: 19:

ZIP: 07601  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/018,635  
FILING DATE:

## CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: David A. Jackson  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-142 CIP1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-487-5800  
TELEFAX: 201-343-1684  
TELEX: 133521

## INFORMATION FOR SEQ. ID NO: 16:

SEQUENCE CHARACTERISTICS:  
LENGTH: 51 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-018-635-16

Query Match 10.3%; Score 163; DB 4; Length 51;  
Best Local Similarity 54.9%; Pred. No. 3e-10;  
Matches 28; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

Qy 65 LKRGNTFEEDRLIKLSLGNKWSLIGRLPGRTDNEIKNWNTHIRK 115

Db 1 VKKSWTEEDRIIYEAHKLGNRMALIAKLPGRTDINSIKHNWSTMRK 51

RESULT 13  
US-09-018-635-19  
Sequence 19, Application US/09018635  
Patent No. 6297356

## GENERAL INFORMATION:

APPLICANT: de Lange, Titia  
APPLICANT: Broccoli, Dominique  
APPLICANT: Smogorzewska, Agata  
TITLE OF INVENTION: TELOMERE REPEAT BINDING FACTOR AND  
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USE THEREOF  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: KLAUBER & JACKSON  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA

ZIP: 07601  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/018,635  
FILING DATE:  
CLASSIFICATION:

## ATTORNEY/AGENT INFORMATION:

NAME: David A. Jackson  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-142 CIP1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-487-5800  
TELEFAX: 201-343-1684  
TELEX: 133521  
INFORMATION FOR SEQ. ID NO: 19:

Search completed: January 23, 2002, 21:12:49  
Job time: 3017 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 23, 2002, 20:25:27 ; Search time 60.99 Seconds  
(Without alignments) 367.197 Million cell updates/sec

Title: US-09-453-387A-2

Perfect score: 1584  
Sequence: 1 MGRSPCCCEKAHTNKGAATKE.....RMCQNSNSNGFYSCRPIDS 294

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 segs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1584	100.0	294	myb-related protei
2	854.5	53.9	274	myb-related protei
3	768	48.5	257	myb-related protei
4	762	48.1	226	DNA-binding protei
5	756.5	47.8	251	myb-related protei
6	728	46.0	273	myb-related protei
7	723	45.6	282	myb-related transc
8	717	45.3	282	myb-related transc
9	704.5	44.5	232	myb-related protei
10	702	44.3	246	probable transcrip
11	693	43.8	235	myb-related protei
12	684	43.2	274	myb-related protei
13	683	43.1	239	myb-related protei
14	683	43.0	267	myb-related protei
15	681.5	43.0	269	probable MYB fami
16	652	41.2	276	myb-related protei
17	626.5	39.6	226	myb-related protei
18	584.5	36.9	332	protein F1504.43
19	567	35.8	325	probable transcrip
20	549.5	34.7	282	probable transcrip
21	546.5	34.5	274	myb-related transc
22	543	34.3	414	hypothetical prote
23	537	33.9	368	myb protein - rice
24	534.5	33.7	324	MYB-like protein
25	533.5	33.7	326	myb-related protei
26	530	33.5	282	hypothetical protei
27	528.5	33.4	352	myb-related protei
28	528	33.3	421	myb-related protei
29	526	33.2	314	probable DNA-bindi

30	524	33.1	249	1	S66688	myb-related protei
31	522	33.0	299	2	T47917	probable transcrip
32	520.5	32.9	369	2	T01196	transcription fact
33	518.5	32.7	336	2	T51644	probable transcrip
34	517.5	32.7	352	2	T51659	myb-related transc
35	515.5	32.5	334	2	T50816	probable transcrip
36	515.5	32.5	371	2	T00438	probable MYB fami
37	514	32.4	453	2	T09745	myb-related protei
38	513	32.4	333	2	G96768	protein transcrip
39	511.5	32.3	371	2	T51636	myb-related transc
40	510	32.2	365	2	D66470	hypothetical prote
41	509	32.1	278	2	T51641	myb-related transc
42	509	32.1	421	1	S24244	myb-related protei
43	507.5	32.0	249	2	E84717	probable MYB fami
44	507.5	32.0	263	2	T48607	probable transcrip
45	505.5	31.9	343	2	T48050	probable transcrip

## ALIGNMENTS

RESULT 1.  
T09879  
myb-related protein A - upland cotton  
C:Species: Gossypium hirsutum (upland cotton)  
C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 26-Aug-1999  
C:Accession: T09879  
R:Wilkins, T.A.; Lu, C.C.  
Submitted to the EMBL Data Library, January 1994  
A:Reference number: Z16894  
A:Accession: T09879  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-294 <WILD>  
A:Cross-references: EMBL:L04497; NID:g437326; PID:g437327  
C:Genetics:  
A:Gene: MYB A  
C:Superfamily: barley myb-related protein 1; myb DNA-binding repeat homology  
C:Keywords: DNA binding; transcription regulation  
F:62-112/Domain: myb DNA-binding repeat homology <MYB>

Query Match	Best Local Similarity	Score	Pred. No.	DB 2:	Length	Matches	Conservative	Mismatches	Indels	Gaps
1	100.0%	1584	294	1	294	294	0	0	0	0
1	MGRSPCCCEKAHTNKGAATKEEDQRLINIRVHGGCWRSLPKAAGLRGCKSRLRWINY	60								
1	MGRSPCCCEKAHTNKGAATKEEDQRLINIRVHGGCWRSLPKAAGLRGCKSRLRWINY	60								
61	LRPDIKRGNTFEEDLLIKLSLGNKMSLIAGRLPGRDNEIKNYWNTHIKRKLISRG	120								
61	LRPDIKRGNTFEEDLLIKLSLGNKMSLIAGRLPGRDNEIKNYWNTHIKRKLISRG	120								
121	IDPQHRPLNQTANTVTVAAPFLDFRNSPTYSKSSSINKPSLDIFYNEFOFSNTPSL	180								
121	IDPQHRPLNQTANTVTVAAPFLDFRNSPTYSKSSSINKPSLDIFYNEFOFSNTPSL	180								
181	EBPNCATSSAGMTDEEQDQLHKQOYGPNGQDINLELSIGIYSADSRVSNANSASEK	240								
181	EBPNCATSSAGMTDEEQDQLHKQOYGPNGQDINLELSIGIYSADSRVSNANSASEK	240								
241	PRVDNNNFQLEQAVAKAVCLQWJGFGTSEICRNCQNSNSNGFYSCRPIDS	294								
241	PRVDNNNFQLEQAVAKAVCLQWJGFGTSEICRNCQNSNSNGFYSCRPIDS	294								

R.Jackson, D.; Cullanez-Macia, F.; Prescott, A.G.; Roberts, K.; Martin, C.  
Plant Cell 3, 115-125, 1991  
A:Title: Expression patterns of myb genes from Antirrhinum flowers.  
A:Reference number: J00956; MUID:93005689  
A:Accession: J00957

A:Molecule type: mRNA  
A:Residues: 1-274 <JAC>  
A:Experimental source: strain J1:522  
C:Superfamily: barley myb-related protein 1; myb DNA-binding repeat homology  
C:Keywords: DNA binding; duplication; nucleus; transcription regulation  
F:9-61/Domain: myb DNA-binding repeat homology <MYB1>  
F:62-112/Domain: myb DNA-binding repeat homology <MYB2>

Query Match 53.9%; Score 854.5; DB 1; Length 274;  
Best Local Similarity 60.5%; Pred. No. 7.6e-57;  
Matches 178; Conservative 23; Mismatches 68; Indels 25; Gaps 8;

QY 1 MGRSPCEKAHTNKGAWTKEEDQRLINIRVHGGCWSLPPRAAGLLRCGKSCRLRWNY 60  
DB 1 MGRSPCEKAHTNKGAWTKEEDQRLINIRVHGGCWSLPPRAAGLLRCGKSCRLRWNY 60  
QY 61 LRDLKRGNTFEEDDELIIKLSLGNKWSLIGRLPGRTDNEIKYNTWHIKRKLISRG 120  
DB 61 LRDLKRGNTFEEDDELIIKLSLGNKWSLIGRLPGRTDNEIKYNTWHIKRKLISRG 120  
QY 121 IDPQTHRLNQTANTNTVTAPE---LDFRNSPTSVSKSSIKNPSLDENEFQFSN 176  
DB 121 IDPQTHRLNQTANTNTVTAPE---LDFRNSPTSVSKSSIKNPSLDENEFQFSN 176  
QY 177 TDSLEPNCATSSGWTDEEQEQLHKQOYGPSNGODINLELSIGIVSADSSRVSNANS 236  
DB 171 SSSSTDPTCKNSS---TTEESQSLITPPKREKESVPLVDLSLGLPSQSCNKSIVSLN 226  
QY 237 AESKPKVDNNFQLEQAMAKAVCLC-WQLGFGTSEICRNQNSNKGFTSIC 289  
DB 227 SSSSGFYD---LFRPPAKVAQRMCVCWTLGLQKGEQFCNQ--SFGNFTYRC 274

## RESULT 3

myb-related protein T22J18.19 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 22-Oct-1999  
A:Accession: T00780  
R:Vygotskaya, V.S.; Schwartz, J.R.; Tortum, M.; Yu, G.; Oji, O.; Kwan, A.; Liu, S.; Li, Tz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, R.  
Submitted to the EMBL Data Library, July 1998  
A:Description: Arabidopsis thaliana chromosome 1 BAC T22J18 sequence, complete sequence.  
A:Reference number: 214202  
A:Accession: T00780  
A:Status: translated from GB/EMBL/DBD  
A:Molecule type: DNA  
A:Residues: 1-257 <YVS>  
A:Cross-references: EMBL:AC003979; NID:g3172156; PIDN:AAC25522.1; PID:g32694; GSPDB:GN00  
A:Experimental source: cultivar Columbia  
C:Genetics:  
A:Gene: ATSP.T22J18.19  
A:Map position: 1  
A:Insertions: 45/1; 88/2  
C:Superfamily: barley myb-related protein 1; myb DNA-binding repeat homology  
C:Keywords: DNA binding; duplication; nucleus; transcription regulation  
F:9-61/Domain: myb DNA-binding repeat homology <MYB1>  
F:62-112/Domain: myb DNA-binding repeat homology <MYB2>

Query Match 48.5%; Score 768; DB 2; Length 257;  
Best Local Similarity 55.6%; Pred. No. 2.1e-50;  
Matches 160; Conservative 33; Mismatches 53; Indels 42; Gaps 7;

QY 1 MGRSPCEKAHTNKGAWTKEEDQRLINIRVHGGCWSLPPRAAGLLRCGKSCRLRWNY 60  
DB 1 MGRSPCEKAHTNKGAWTKEEDQRLINIRVHGGCWSLPPRAAGLLRCGKSCRLRWNY 60

QY 61 LRDLKRGNTFEEDDELIIKLSLGNKWSLIGRLPGRTDNEIKYNTWHIKRKLISRG 120  
DB 61 LRDLKRGNTFEEDDELIIKLSLGNKWSLIGRLPGRTDNEIKYNTWHIKRKLISRG 120  
QY 121 IDPQTHRLNQTANTNTVTAPELDFRNSPTSVSKSSIKNPSLDENEFQFSNDSL 180  
DB 121 IDPQTHRLNQTANTNTVTAPELDFRNSPTSVSKSSIKNPSLDENEFQFSNDSL 180  
QY 181 EEP---NCTASSGWTDEEQEQLHKQOYGPSNGODINLELSIG-IVSADSSR-VSN 233  
DB 161 REELGMVNNC-ESSGTTSEKD-----YNEEDVUINLELSVSPSTYRESTRKYSV 209  
QY 234 ANSAEKPKVDNNFQLEQAMAKAVCLC-WQLGFGTSEICRNQNSN 281  
DB 210 VDSAESTRWSELF---GAHESDAVLCRCRGLFRNESCRNCRVSD 253

## RESULT 4

D85096  
DNA-binding protein [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 02-Mar-2001  
A:Accession: D85096  
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Nature 402, 769-777, 1999  
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
A:Reference number: A85001; MUID:20083488  
A:Accession: D85096  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-236 <STO>  
A:Cross-references: GB:NC\_001268; NID:g7267641; PIDN:CA878069.1; GSPDB:GN00140  
C:Genetics:  
A:Gene: AT4G09460  
A:Map position: 4  
C:Superfamily: Arabidopsis myb-related protein 5; myb DNA-binding repeat homology

Query Match 48.1%; Score 762; DB 2; Length 236;  
Best Local Similarity 58.9%; Pred. No. 5.3e-50;  
Matches 145; Conservative 39; Mismatches 40; Indels 22; Gaps 5;

QY 1 MGRSPCEKAHTNKGAWTKEEDQRLINIRVHGGCWSLPPRAAGLLRCGKSCRLRWNY 60  
DB 1 MGRSPCEKAHTNKGAWTKEEDQRLINIRVHGGCWSLPPRAAGLLRCGKSCRLRWNY 60  
QY 61 LRDLKRGNTFEEDDELIIKLSLGNKWSLIGRLPGRTDNEIKYNTWHIKRKLISRG 120  
DB 61 LRDLKRGNTFEEDDELIIKLSLGNKWSLIGRLPGRTDNEIKYNTWHIKRKLISRG 120  
QY 121 IDPQTHRLNQTANTNTVTAPELDFRNSPTSVSKSSIKNPSLDENEFQFSNDSL 179  
DB 121 IDPQTHRLNQTANTNTVTAPELDFRNSPTSVSKSSIKNPSLDENEFQFSNDSL 179  
QY 180 LEEPNCATSSGWTDEEQEQLHKQOYGPSNGO-DINLELSIGIVSADSSRVSNANS 238  
DB 164 SSD-NGASTSGTTDEDLQ--NGECYSDNSGHINKINDLLTGLFGWSGRIVGSSAD 220  
QY 239 SKPKVD 244  
DB 221 SKPMCD 226

## RESULT 5

S35729  
myb-related protein 2 - barley  
N:Alternate names: myb2 protein; MybH5 protein  
C:Species: Hordeum vulgare (Barley)  
C>Date: 03-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 18-Jun-1999  
A:Accession: S35729; S31813; S61507  
R:Ronde, W.  
Submitted to the EMBL Data Library, January 1993

A:Reference number: S35419  
A:Accession: S35729  
A:Molecule type: mRNA  
A:Residues: 1-251 <ROH>  
A:Cross-references: EMBL:X70876; NID:g19054; PIDN:CA50221.1; PID:g19055  
R:Wissenbach, M.; Ueberlacker, B.; Vogt, F.; Becker, D.; Salami, F.; Rohde, W.  
Submitted to the EMBL Data Library, January 1993  
A:Description: Myb gene from hordeum vulgare: tissue-specific expression of chimeric Myb  
A:Reference number: S31813  
A:Accession: S31813  
A:Molecule type: DNA  
A:Residues: 1-104 <WIS>  
A:Cross-references: EMBL:X70880; NID:g19056; PIDN:CA50225.1; PID:g19057  
R:Wissenbach, M.; Ueberlacker, B.; Vogt, F.; Becker, D.; Salami, F.; Rohde, W.  
Plant J. 4, 411-422, 1993  
A:Title: Myb genes from Hordeum vulgare: tissue-specific expression of chimeric Myb prom  
A:Reference number: S61507  
A:Accession: S61507  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-117 <W12>  
A:Cross-references: EMBL:X70880  
C:Genetics:  
A:Gene: myb2  
A:Introns: 88/2  
C:Superfamily: barley myb-related protein 1; myb DNA-binding repeat homology  
C:Keywords: DNA binding; duplication; nucleus; transcription regulation  
F:9-61/Domain: myb DNA-binding repeat homology <MYB1>  
F:62-112/Domain: myb DNA-binding repeat homology <MYB2>

Query Match 47.8%; Score 756.5; DB 1; Length 251;  
Best Local Similarity 50.7%; Pred. No. 1.5e-49;  
Matches 152; Conservative 32; Mismatches 55; Indels 61; Gaps 6;

QY 1 MGSPCCERKATNKGAATKEEDQRLINIRVHGECGRSLPKAAGLLRCGKSCRLRWNY 60  
|||||  
DB 1 MGSPCCERKATNKGAATKEEDQRLINIRVHGECGRSLPKAAGLLRCGKSCRLRWNY 60  
1 MGSPCCERKATNKGAATKEEDQRLINIRVHGECGRSLPKAAGLLRCGKSCRLRWNY 60  
QY 61 LRPDLKRGNTFEEDDELIIKLHSLGNKWSLIAGRLPGRTDNEIKNYWTHIRKRLISRG 120  
|||||  
DB 61 LRPDLKRGNTFEEDDELIIKLHSLGNKWSLIAGRLPGRTDNEIKNYWTHIRKRLISRG 120  
QY 121 IDPQTHRLPLNOTANTNTVTAPEL--DFRNSPTSV--SKSSSIKNPSLDNFYNEFOKSNST 177  
|||||  
DB 121 IDPQTHRLPLNOTANTNTVTAPEL--DFRNSPTSV--SKSSSIKNPSLDNFYNEFOKSNST 177  
QY 178 DSLEEFNCTASSGWTDEEQQLHKQOYGPSNGODINLELSIGIVSADSSRVSNANSA 237  
|||||  
DB 181 TSTGEPRC-----PDNLNLDLSVGPADPT----- 205  
QY 238 ESKPKYDNNNFQLEQAMVAKAVLCWOLGFGTSEICRNCQNSNS---NGFSTYCRPLD 293  
|||||  
DB 206 -----TSHPVCLCRHLGFRGEGAC--SCROADSSAGSOGGGRFYRFRPLE 246  
A:Reference number: S69189; MUID:96270378  
A:Accession: S69189  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-273 <LIN>  
A:Cross-references: EMBL:X95296; NID:g1167483; PIDN:CA64614.1; PID:g1167484  
C:Genetics:  
A:Gene: TMH27

C:Superfamily: barley myb-related protein 1; myb DNA-binding repeat homology  
C:Keywords: DNA binding; duplication; nucleus; transcription regulation  
F:9-61/Domain: myb DNA-binding repeat homology <MYB1>  
F:62-112/Domain: myb DNA-binding repeat homology <MYB2>

Query Match 46.0%; Score 728; DB 1; Length 273;  
Best Local Similarity 53.0%; Pred. No. 2.2e-47;  
Matches 151; Conservative 26; Mismatches 64; Indels 44; Gaps 5;

QY 1 MGSPCCERKATNKGAATKEEDQRLINIRVHGECGRSLPKAAGLLRCGKSCRLRWNY 60  
|||||  
DB 1 MGSPCCERKATNKGAATKEEDQRLINIRVHGECGRSLPKAAGLLRCGKSCRLRWNY 60  
QY 61 LRPDLKRGNTFEEDDELIIKLHSLGNKWSLIAGRLPGRTDNEIKNYWTHIRKRLISRG 120  
|||||  
DB 61 LRPDLKRGNTFEEDDELIIKLHSLGNKWSLIAGRLPGRTDNEIKNYWTHIRKRLISRG 120  
QY 121 IDPQTHRLPLNOTANTNTVTAPELDFRNSPTSVSKSSSIKNPSLDNFYNEFOKSNSTDL 180  
|||||  
DB 121 IDPQTHRLPLNOTANTNTVTAPELDFRNSPTSVSKSSSIKNPSLDNFYNEFOKSNSTDL 180  
QY 181 EEPNCTASSGWTDEEQQLHKQOYGPSNGODINLELSIGIVSADSSRVSNANSAESK 240  
|||||  
DB 158 EMINIKAEFVETSKESDNEI--IQKSSSCLDPLNLELI-----SPPH 201  
QY 241 PKVDNNNFQLEQAMVAKAVLCWOLGFGTSEICRNCQNSNSNGF 285  
|||||  
DB 202 QQLDHRHH-----QRSSLCFTCSIGIQNSKSCSGSESGNGW 241

RESULT 7  
T05690  
Myb-related transcription factor MYB4 - Arabidopsis thaliana  
N:Alternate names: protein F20M13.180  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 13-Aug-1999  
R:Bevan, M.; Medler, H.; Kutner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, submitted to the Protein Sequence Database, February 1999  
A:Reference number: Z15420  
A:Accession: T05690  
A:Molecule type: DNA  
A:Residues: 1-282 <BEV>  
A:Cross-references: EMBL:AL035540  
A:Experimental source: cultivar Columbia; BAC clone F20M13  
C:Genetics:  
A:Gene: MYB4  
A:Map position: 4  
A:Introns: 88/2  
A:Note: F20M13.180  
C:Superfamily: barley myb-related protein 1; myb DNA-binding repeat homology  
C:Keywords: DNA binding; duplication; nucleus; transcription regulation  
F:9-61/Domain: myb DNA-binding repeat homology <MYB1>  
F:62-112/Domain: myb DNA-binding repeat homology <MYB2>

Query Match 45.6%; Score 723; DB 2; Length 282;  
Best Local Similarity 52.0%; Pred. No. 5.5e-47;  
Matches 146; Conservative 38; Mismatches 49; Indels 48; Gaps 7;

QY 1 MGSPCCERKATNKGAATKEEDQRLINIRVHGECGRSLPKAAGLLRCGKSCRLRWNY 60  
|||||  
DB 1 MGSPCCERKATNKGAATKEEDQRLINIRVHGECGRSLPKAAGLLRCGKSCRLRWNY 60  
QY 61 LRPDLKRGNTFEEDDELIIKLHSLGNKWSLIAGRLPGRTDNEIKNYWTHIRKRLISRG 120  
|||||  
DB 61 LRPDLKRGNTFEEDDELIIKLHSLGNKWSLIAGRLPGRTDNEIKNYWTHIRKRLISRG 120  
QY 121 IDPQTHRLPLNOTANTNTVTAPELDFRNSPT--SVKSSSIKNPSLDNFYNEFOKSNSTDS 179  
|||||  
DB 121 IDPQTHRLPLNOTANTNTVTAPELDFRNSPT--SVKSSSIKNPSLDNFYNEFOKSNSTDS 176

QY 180 LEEPNCTASSGTTDEEQEOLHKQOYGPSNGODINLEL----- 219  
 DB 177 I-----SMLTFKEEKEDECPVQEKF-----PDLNLELISLPDDVDRLQGHGKSTTP 222  
 QY 220 -----SIGIVSADSSRVSNAN-----SAESKPKVNNNFQFL 251  
 DB 223 RCFKCSLGMINGMECHRCGRMCDVYGGSSKGSMDSNDFL 263

RESULT 8  
 T51632  
 myb-related transcription factor MYB4 [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 18-Aug-2000 #sequence\_rev18-Aug-2000 #text\_change 02-Sep-2000  
 C:Accession: T51632  
 R:Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.; J  
 ; Paz-Ares, J.; Weisshaar, B.  
 Plant J. 16, 263-276, 1998  
 A:Title: Towards functional characterisation of the members of the R2R3-MYB gene from Ar  
 A:Reference number: Z14349; MUID:9839469  
 A:Accession: T51632  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-262 <KRA>  
 A:Cross-references: EMBL:AF062860; PIDN:AAC83582.1  
 A:Experimental source: cultivar Columbia  
 C:Genetics:  
 A:Gene: MYB4  
 C:Superfamily: barley myb-related protein 1; myb DNA-binding repeat homology

Query Match 45.3%; Score 717; DB 2; Length 282;  
 Best Local Similarity 51.6%; Pred. No. 1.6e-46;  
 Matches 145; Conservative 38; Mismatches 50; Indels 48; Gaps 7;

QY 1 MGRSPCCERKATNKGAATKEEDORLNIYIRVHGECCWRSPLPKAGLLRCGKSCRLRWINY 60  
 DB 1 MGRSPCCERKATNKGAATKEEDORLNIYIRVHGECCWRSPLPKAGLLRCGKSCRLRWINY 60  
 QY 61 LRPDLKRGNTFEEDEELIKLHSLGKMSLIAGRLPGRTDNEIKNWNTHIRKRLISRG 120  
 DB 61 LRPDLKRGNTFEEDEELIKLHSLGKMSLIAGRLPGRTDNEIKNWNTHIRKRLISRG 120  
 QY 121 IDPOTHRPLNQTANTNTVTAFTLEDFRNSPT-SYKSSSINKPSLDFVNEFOFKSNTDS 179  
 DB 121 IDPOTHRPLNQTANTNTVTAFTLEDFRNSPT-SYKSSSINKPSLDFVNEFOFKSNTDS 179  
 QY 180 LEEPNCTASSGTTDEEQEOLHKQOYGPSNGODINLEL----- 219  
 DB 177 I-----SMLTFKEEKEDECPVQEKF-----PDLNLELISLPDDVDRLQGHGKSTTP 222  
 QY 220 -----SIGIVSADSSRVSNAN-----SAESKPKVNNNFQFL 251  
 DB 223 RCFKCSLGMINGMECHRCGRMCDVYGGSSKGSMDSNDFL 263

RESULT 9  
 J009607  
 myb-related protein 308 - garden snapdragon  
 C:Species: Antirrhinum majus (garden snapdragon)  
 C:Date: 30-Sep-1991 #sequence\_rev18-Aug-1991 #text\_change 24-Jul-1997  
 C:Accession: J009607  
 R:Jackson, D.; Cullane, M.; Prescott, A.G.; Roberts, K.; Martin, C.  
 Plant Cell 3, 115-125, 1991  
 A:Title: Expression patterns of myb genes from Antirrhinum flowers.  
 A:Reference number: J00936; MUID:93005689  
 A:Accession: J009607  
 A:Molecule type: mRNA  
 A:Residues: 1-232 <JAC>  
 A:Experimental source: strain J1-522  
 C:Comment: The gene encoding for this protein is expressed in all plant organs.  
 C:Superfamily: barley myb-related protein 1; myb DNA-binding repeat homology  
 C:Keywords: DNA binding; duplication; nucleus; transcription regulation

F:9-61/Domain: myb DNA-binding repeat homology <MYB1>  
 F:62-112/Domain: myb DNA-binding repeat homology <MYB2>

Query Match 44.5%; Score 704.5; DB 1; Length 232;  
 Best Local Similarity 52.4%; Pred. No. 1.1e-45;  
 Matches 150; Conservative 24; Mismatches 55; Indels 57; Gaps 8;

QY 1 MGRSPCCERKATNKGAATKEEDORLNIYIRVHGECCWRSPLPKAGLLRCGKSCRLRWINY 60  
 DB 1 MGRSPCCERKATNKGAATKEEDORLNIYIRVHGECCWRSPLPKAGLLRCGKSCRLRWINY 60  
 QY 61 LRPDLKRGNTFEEDEELIKLHSLGKMSLIAGRLPGRTDNEIKNWNTHIRKRLISRG 120  
 DB 61 LRPDLKRGNTFEEDEELIKLHSLGKMSLIAGRLPGRTDNEIKNWNTHIRKRLISRG 120  
 QY 121 IDPOTHRPLNQTANTNTVTAFTLEDFRNSPT-SYKSSSINKPSLDFVNEFOFKSNTDS 179  
 DB 121 IDPOTHRPLNQTANTNTVTAFTLEDFRNSPT-SYKSSSINKPSLDFVNEFOFKSNTDS 179  
 QY 180 LEEPNCTASSGTTDEEQEOLHKQOYGPSNGO--DINLELSIGIVSADSSRVSNANSA 237  
 DB 150 KEE-----DTKHKAVADIMIKENSPVQERCPDNLDTKI---SPCCQOQINTHOE 197  
 QY 238 ESKPKVDNNNFQFLQAVAKAVCLQWLGFTSEICRNCQNSN 283  
 DB 198 NLKTGGRNG-----SPTLCFVCRIGIQNSKDC-SCSDGVGN 232

RESULT 10  
 T51631  
 Probable transcription factor MYB3 [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 18-Aug-2000 #sequence\_rev18-Aug-2000 #text\_change 02-Sep-2000  
 C:Accession: T51631  
 R:Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.  
 ; Paz-Ares, J.; Weisshaar, B.  
 Plant J. 16, 263-276, 1998  
 A:Title: Towards functional characterisation of the members of the R2R3-MYB gene fr  
 A:Reference number: Z14349; MUID:9839469  
 A:Accession: T51631  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-246 <KRA>  
 A:Cross-references: EMBL:AF062859; PIDN:AAC83581.1  
 A:Experimental source: cultivar Columbia  
 C:Genetics:  
 A:Gene: MYB3  
 C:Superfamily: barley myb-related protein 1; myb DNA-binding repeat homology

Query Match 44.3%; Score 702; DB 2; Length 246;  
 Best Local Similarity 54.0%; Pred. No. 1.7e-45;  
 Matches 149; Conservative 33; Mismatches 52; Indels 42; Gaps 7;

QY 13 NKGAMTKEDORLNIYIRVHGECCWRSPLPKAGLLRCGKSCRLRWINYLRPDLKRGNTF 72  
 DB 2 NKGAMTKEDORLNIYIRVHGECCWRSPLPKAGLLRCGKSCRLRWINYLRPDLKRGNTF 61  
 QY 73 EDELLIKLHSLGKMSLIAGRLPGRTDNEIKNWNTHIRKRLISGIDPQTHRLNQT 132  
 DB 62 EDELLIKLHSLGKMSLIAGRLPGRTDNEIKNWNTHIRKRLISGIDPQTHRLNQT 120  
 QY 133 ANTNTVTAFTLEDFRNSPT-SYKSSSINKPSLDFVNEFOFKSNTDSLEBP-----NCTA 187  
 DB 121 -----SVSPSSLQNDVYETHLDSGPVPEPVREIGAVNMC-E 160  
 QY 188 SSGMTTDEEQEOLHKQOYGPSNGODINLELSIG-IVSADSSR-VSNANSAESKPKVDN 245  
 DB 161 SSGTSEKD-----YGNEDMVNLDELISVGSYKRESTRKYSVDSABSTRMGS 210  
 QY 246 NNQFLQAVAKAVCLQWLGFTSEICRNCQNSN 281





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 23, 2002, 21:12:53 ; Search time 51.05 Seconds  
(without alignments)  
211.155 Million cell updates/sec

File: US-09-453-387a-2

Perfect score: 1584  
Sequence: 1 MGRSPCEKAHTNGAWTKE.....RNCNSNSNGFYSCRLPDS 294

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	693	43.8	255	1 MYB3_MAIZE	P20025 zea mays (m
2	683	43.1	267	1 MYB1_HORVU	P20026 hordeum vul
3	509	32.1	421	1 MYB2_PHYPA	P80073 physcomitre
4	496.5	31.3	399	1 MYBP_MAIZE	P27898 zea mays (m
5	490	30.9	340	1 MYB1_MAIZE	P20024 zea mays (m
6	454.5	28.0	302	1 MYB3_HORVU	P20027 hordeum vul
7	443.5	28.0	273	1 MYBC_MAIZE	P10590 zea mays (m
8	439	27.7	252	1 MYBD_MAIZE	P23592 zea mays (m
9	402.5	25.4	228	1 G11_ARATH	P27900 arabidopsis
10	332	20.3	382	1 MYB_AVIMB	P01104 avian myelo
11	312	19.7	686	1 MYBB_CHICK	P03337 gallus gall
12	309	19.5	728	1 MYBA_CHICK	P05935 xenopus lae
13	306.5	19.3	743	1 MYBB_XENLA	P52551 xenopus lae
14	304.5	19.2	704	1 MYBB_MOUSE	P48972 mus musculu
15	303	19.1	641	1 MYB_CHICK	P01103 gallus gall
16	300	18.9	640	1 MYB_BOVIN	P46200 bos taurus
17	299.5	18.9	700	1 MYBB_HUMAN	P10242 homo sapien
18	296	18.7	451	1 MYBH_DICDI	P34127 dictyostell
19	296	18.7	640	1 MYB_HUMAN	P10242 homo sapien
20	294	18.6	636	1 MYB_MOUSE	P06876 mus musculu
21	291	18.4	751	1 MYBA_MOUSE	P51660 mus musculu
22	288.5	18.2	624	1 MYB_XENLA	P08759 xenopus lae
23	288.5	18.2	752	1 MYBA_HUMAN	P10243 homo sapien
24	284	17.9	757	1 MYBA_CHICK	P52550 gallus gall
25	274	17.3	657	1 MYB_DROME	P04197 drosophil
26	274	17.3	449	1 MYB1_PHYPA	P80074 physcomitre
27	160	10.1	811	1 BAS1_YEAST	P22035 saccharomyc
28	133	8.4	590	1 Y63_YEAST	P03654 saccharomyc
29	132	8.3	757	1 CCS_SCHPO	P39964 schizosacch
30	117	7.4	810	1 REB1_YEAST	P21598 saccharomyc
31	110	6.9	595	1 REB1_KLULA	P03950 kluyveromyc
32	106	6.7	534	1 GCR2_YEAST	P01722 saccharomyc
33	102.5	6.5	661	1 WHI3_YEAST	P34761 saccharomyc

34	102.5	6.5	730	1 GLN3_YEAST	P18494 saccharomyc
35	102	6.4	696	1 SKT5_YEAST	P34226 saccharomyc
36	99.5	6.3	1113	1 PER3_MOUSE	P070361 mus musculu
37	98.5	6.2	410	1 IMP2_CRIGR	P49130 cricetus
38	98	6.2	923	1 YEL2_YEAST	P40017 saccharomyc
39	96.5	6.1	652	1 DYN1_DICDI	P54703 dictyostell
40	95.5	6.0	1373	1 HRP1_SCHPO	P09425 schizosacch
41	94.5	6.0	781	1 Y3B_YEAST	P53316 saccharomyc
42	94.5	6.0	1704	1 VIR1_FUNHE	P090508 fundulus he
43	93.5	5.9	1142	1 POL_HVZBE	P18096 human immun
44	93.5	5.9	1822	1 Y6B_CAEEL	P34529 caenorhabdi
45	92.5	5.8	382	1 MSN1_YEAST	P22148 saccharomyc

## ALIGNMENTS

RESULT ID	MYB3_MAIZE	STANDARD	PRT	255 AA.
AC	P20025;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	01-OCT-1996 (Rel. 34, Last annotation update)			
DE	MYB-RELATED PROTEIN ZM38.			
OS	Zea mays (Maize).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;			
OC	Panicoidae; Andropogoneae; Zea.			
OX	NCBI_TaxID=4577;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89313655; PubMed=266447;			
RA	Matrocco A., Wassenbach M., Becker D., Paz-Ares J., Siedler H.,			
RA	Saladini F., Rohde W.;			
RT	"Multiple genes are transcribed in Hordeum vulgare and Zea mays that			
RT	carry the DNA binding domain of the myb oncoproteins."			
RL	Mol. Gen. Genet. 216:183-187(1989).			
CC	1- SIMILARITY: BELONGS TO THE MYB FAMILY.			
DR	PIR: S04899; S04899.			
DR	HSSP: P01103; IPOM.			
DR	MaizeDB: 69594;			
DR	InterPro: IPR001005; MYB_DNA_bind.			
DR	Pfam: PF00249; myb_DNA-binding; 2.			
DR	SMART: SM00395; SANT: 2.			
DR	PROSITE: PS00037; MYB_1; 1.			
DR	PROSITE: PS00334; MYB_2; 1.			
DR	PROSITE: PS50090; MYB_3; 2.			
KW	Nuclear protein; DNA-binding; Repeat; Transcription regulation.			
FT	DNA_BIND 9 61 MYB.			
SO	SEQUENCE 255 AA; 27568 MW; 26AADC8B0633E06 CRC64;			

Query Match	43.8%; Score 693; DB 1; Length 255;
Best Local Similarity	47.1%; Pred. No. 3.4e-46;
Matches 140; Conservative 33; Mismatches 50; Indels 74; Gaps 7;	
OY	1 MGRSPCEKAHTNGAWTKEEDORLIVIRYHSGCWRSLKRAAGLACGSCRLRWNY 60
DB	1 MGRSPCEKAHTNGAWTKEEDORLIVIRYHSGCWRSLKRAAGLACGSCRLRWNY 60
OY	61 LRPDLKRGNTAEDEDLIVLHSLGKMSLIAGRLPGRTNENIKYNTHTKRLISRG 120
DB	61 LRPDLKRGNTAEDEDLIVLHSLGKMSLIAGRLPGRTNENIKYNTHTKRLISRG 120
OY	121 IDPOTHRPNTANTVTAPELDFRNSPTSVSKSSIKNPISLDFNENEFKSNITDSL 180
DB	121 IDPOTHRPNTANTVTAPELDFRNSPTSVSKSSIKNPISLDFNENEFKSNITDSL 180
OY	181 EEPNCTASSGTTDEEQOELHKKOYGPSNGQINLELSIGIYSADSSRYNANSAESK 240
DB	181 EEPNCTASSGTTDEEQOELHKKOYGPSNGQINLELSIGIYSADSSRYNANSAESK 240
OY	161 KAPRC-----PDLNLDLCI-----SPCQOQOEEBEVDK 189
DB	161 KAPRC-----PDLNLDLCI-----SPCQOQOEEBEVDK 189

DB	190	PSA	-----	AVVREVLGGRGHGHCALCFCCSLGVOKGAPGCCSSSSNG	236
OY	241	PKYVNNNNFOEADMAKAV	-----	CLCWLQGLGTEIEICRNQNSNSNG	284
DT	01-FEB-1991	(Rel. 17, Created)			
DT	01-FEB-1991	(Rel. 17, Last sequence update)			
DT	01-OCT-1996	(Rel. 34, Last annotation update)			
DE	MYB-RELATED PROTEIN HV1.				
GN	MYB1.				
OS	Hordeum vulgare (Barley).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;				
OX	Triliceae; Hordeum.				
OX	NCBI_TaxID=4513;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-CV. ABYSSINIAN 2231;				
RX	MEDLINE=69313655; Pubmed=2664447;				
RA	Marocco A., Wiesenbach M., Becker D., Paz-Ares J., Saedler H.,				
RA	Salamini F., Rohde W.;				
RT	"Multiple genes are transcribed in Hordeum vulgare and Zea mays that				
RT	carry the DNA binding domain of the myb oncoproteins.";				
RL	Mol. Gen. Genet. 216:183-187(1989).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-CV. ABYSSINIAN 2231; TISSUE=Leaf;				
RX	MEDLINE=94035190; Pubmed=8220488;				
RA	Wiesenbach M., Ueberlacker B., Vogt F., Becker D., Salamini F.,				
RA	Rohde W.;				
RT	"Myb genes from Hordeum vulgare: tissue-specific expression of				
RT	chimeric Myb promoter/Gus genes in transgenic tobacco.";				
RL	Plant J. 4:411-422(1993).				
CC	-1- FUNCTION. POSSIBLE TRANSCRIPTION ACTIVATOR IN RESPONSE TO AN				
CC	EXTERNAL SIGNAL. MAY BE INVOLVED IN THE REGULATION OF FLAVONOID				
CC	BIOSYNTHESIS.				
CC	-1- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).				
CC	-1- TISSUE SPECIFICITY: GERMINATING SEED AND APICAL MERISTEM OF SHOOT				
CC	AND ROOT.				
CC	-1- SIMILARITY: BELONGS TO THE MYB FAMILY.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	CC or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
CC	-----				
DR	EMBL; X70877; CA50222.1;				
DR	EMBL; X70879; CA50224.1;				
DR	PIR; S04896; S04896.				
DR	PIR; S31817; S31817.				
DR	HSSP; P01103; IPOM.				
DR	Mendel; 8594; HORVU; MYB; m8594.				
DR	InterPro; IPR001005; MYB_DNA_bind.				
DR	Pfam; PF00249; myb_DNA-binding; 2.				
DR	SMART; SMO0395; SANT; 2.				
DR	PROSITE; PS00037; MYB_1; 1.				
DR	PROSITE; PS00334; MYB_2; 1.				
DR	PROSITE; PS50090; MYB_3; 2.				
KW	Nuclear protein; DNA-binding; Activator; Transcription regulation;				
KW	Repeat.				
FT	DNA_BIND	9	61	MYB.	
FT	DNA_BIND	62	102	MYB.	
SO	SEQUENCE	267 AA;	29740 MW;	DECEDCCEBA847749 CRC64;	

	Query Match	43.1%; Score 683; DB 1; Length 267;
	Best Local Similarity	50.7%; Pred. No. 2.Le-45;
	Matches 142; Conservative	28; Mismatches 72; Indels 38; Gaps 5
QY	1	MGRSPCEKAKHTNGAMWKEEDORLINTIRVAGECBSMSLPKAAGILRCKGSCRLLRWINY 60
DB	1	MGRSCECKAKHTNGAMWKEEDDRLTATIKAGBECBSMSPRAAGILRCKGSCRLLRWINY 60
QY	61	LRPDLKRGNTFEDEDELIIKLHSLLGNNKWSLIAGRPGRTDNEIKNYWTHIRKRLITSRG 120
DB	61	LRPDLKRGNFSHEDELIIKLHSLLGNNKWSLIAGRPGRTDNEIKNYWTHIRKRLITSRG 120
QY	121	IDPQCHREPLNOTANTNTYTAPTELDPRFNSPTVSYSKSSSTLNKPSLDPNRYNEFOFKSTBDL 180
DB	121	IDPVTHRAINSNDHAASNTISFEESAQORDKGAVFR-----RDAAE 159
QY	181	EHPNCTAASSGMTTDEEOEQQLHKKOQYG---PSNQDITLIELSIGIVASDSSRYANANA 237
DB	160	PAKAAAAAAAISHVDHHHSRNPODLWGOGKGLKCPDLNLIDLCI-----SPPIHEDPNV 213
QY	238	ESKPEVDNNNFOLFEOAWYAKAVCLCW--OLGFGTSEICR 275
DB	214	DTKPYVKR-----EAGYGVGVGVLGTCSCSMGLPPRSSDCK 247

ID	MYB2_PHYPA	STANDARD;	PRT;	421 AA.
AC	P80073;			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	01-OCT-1996 (Rel. 34, Last annotation update)			
DE	MYB-RELATED PROTEIN PP2.			
GN	PP2.			
OS	Physcomitrella patens (Moss).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;			
CC	Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.			
RX	NCBI_TaxID=3218;			
LN	(1)			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94004988; PubMed=8401607;			
RA	Leech M.J., Kammerer W., Cove D.J., Martin C., Wang T.L.;			
RT	"Expression of myb-related genes in the moss, Physcomitrella patens."			
RL	Plant J 3:51-61(1993).			
CC	-1- FUNCTIONAL: POSSIBLE TRANSCRIPTION ACTIVATOR.			
CC	-1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).			
CC	-1- DEVELOPMENTAL STAGE: HIGH RATES OF GROWTH.			
CC	-1- SIMILARITY: BELONGS TO THE MYB FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL; X67050; CAA47435.1; -			
DR	PIR; S24244; S24244.			
DR	HSSP; P01103; IPOM.			
DR	Interpro: IPR001005; Myb.DNA_bind.			
DR	Pfam: PR000249; myb.DNA-binding; 2.			
DR	SMART; SM00393; SANT; 2.			
DR	PROSITE; PS00037; MYB_1; 1.			
DR	PROSITE; PS00334; MYB_2; 1.			
DR	PROSITE; PS50090; MYB_3; 2.			
KW	Nuclear protein; DNA-binding; Repeat; Transcription regulation.			
FT	DNA_BIND 9 61 MYB.			
FT	DNA_BIND 62 102 MYB.			
FT	SEQUENCE 421 AA; 46695 MW; 27A35785F8D0F3F4 CRC64;			

Query Match 32.1%; Score 509; DB 1; Length 421;



Best Local Similarity 55.8%; Pred. No. 7.5e-32;  
Matches 91; Conservative 27; Mismatches 45; Indels 0; Gaps 0;

QY 1 MGRSPCCERAHNKGAWTEEDORLNIYRVHGGCWRSLPKAGLLRCGSCRLRMVY 60  
DB 1 MGRKPCCEKVGKRGWTEEDQKLVSHITNNGSWRAIPKLGKCGSCRLRMVY 60  
QY 61 LRPDLKRGNTFEEDLLIKLHSLGKNSLGRPLGRTDNEIKNYNTHIRKRLISRG 120  
DB 61 LRPDLKRGNTFEEDLLIKLHSLGKNSLGRPLGRTDNEIKNYNTHIRKRLISRG 120  
QY 121 IDPQTHPLNQTANTNTVTAPELDFRNSPTSVSKSSIKNPS 163  
DB 121 IDPQTHPLNQTANTNTVTAPELDFRNSPTSVSKSSIKNPS 163

RESULT 4  
MYB\_MAIZE  
ID MYB\_MAIZE STANDARD; PRT; 399 AA.  
AC P27898; P27899;  
DT 01-AUG-1992 (rel. 23, Created)  
DT 01-AUG-1992 (rel. 23, Last sequence update)  
DT 15-JUL-1999 (rel. 38, Last annotation update)  
DE MYB-RELATED PROTEIN P.  
GN P.  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;  
OC Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91271238; PubMed=2052542;  
RA Groenewald E., Peterson T.;  
RT "Alternatively spliced products of the maize P gene encode proteins with homology to the DNA-binding domain of myb-like transcription factors.";  
RT Proc. Natl. Acad. Sci. U.S.A. 88:4587-4591(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92275319; PubMed=1317315;  
RA Athma P., Groenewald E., Peterson T.;  
RT "Insertional mutagenesis of the maize P gene by intragenic transposition of Ac.";  
RT Genetics 131:199-209(1992).  
CC -1- FUNCTION: TRANSCRIPTION FACTOR POSTULATED TO REGULATE THE BIOSYNTHETIC PATHWAY OF A FLAVONOID-DERIVED PIGMENT IN CERTAIN FLORAL TISSUES.  
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -1- SIMILARITY: BELONGS TO THE MYB FAMILY.  
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CC  
DR EMBL; M73028; AAA33500.1; -;  
DR EMBL; M73029; AAA33501.1; -;  
DR EMBL; Z11879; CAA77939.1; -;  
DR PIR; A39697; A39697.  
DR PIR; B39697; B39697.  
DR PIR; S26150; S26150.  
DR HSSP; P01103; 1POM.  
DR TRANSFAC; T01580; -;  
DR TRANSFAC; T01591; -;  
DR MaizeDB; 69180; -;  
DR MaizeDB; 69181; -;  
DR InterPro; IPR001005; MYB\_DNA\_bind.  
DR Pfam; PF00249; myb\_DNA-binding; 2.

DR SMART; SM00395; SANT; 2.  
DR PROSITE; PS00037; MYB\_1; 1.  
DR PROSITE; PS00334; MYB\_2; 1.  
DR PROSITE; PS00090; MYB\_3; 2.  
KW Nuclear protein; DNA-binding; Repeat; Transcription regulation;  
KW Alternative splicing.  
FT DNA\_BIND 9 61  
FT MYB.  
FT DNA\_BIND 62 102  
FT DOMAIN 178 181  
FT POLY-ALA.  
FT POLY-LEU.  
FT VARSPIC 89 152  
FT WSLIASHLPGRDNEIKNYNTHIRKRLISRG  
FT TAIATDMSKLSADRGRGRTRG -> RHIMIRAKYRAGPD  
FT VACPLGALATLPLRQSPPTARTATYDRIGSALLRSVRC  
FT FRCSVSRW (IN SHORT ISOFORM).  
FT MISSING (IN SHORT ISOFORM).  
FT VARSPIC 153 399.  
FT MISSING (IN SHORT ISOFORM).  
SQ SEQUENCE 399 AA; 43756 MW; EEO25B00A44CF5D0 CRC64;

Query Match 31.3%; Score 496.5; DB 1; Length 399;  
Best Local Similarity 42.7%; Pred. No. 6.3e-31;  
Matches 103; Conservative 25; Mismatches 56; Indels 57; Gaps 4;

QY 1 MGRSPCCERAHNKGAWTEEDORLNIYRVHGGCWRSLPKAGLLRCGSCRLRMVY 60  
DB 1 MGRKPCCEKVGKRGWTEEDQKLVSHITNNGSWRAIPKLGKCGSCRLRMVY 60  
QY 61 LRPDLKRGNTFEEDLLIKLHSLGKNSLGRPLGRTDNEIKNYNTHIRKRLISRG 118  
DB 61 LRPDLKRGNTFEEDLLIKLHSLGKNSLGRPLGRTDNEIKNYNTHIRKRLISRG 118  
QY 119  
DB 119  
QY 121 RKYTGPDPTAIDMSKLSADRGRGRTRGPRASARTQADADPGEGAKGPAA 180  
DB 121 RKYTGPDPTAIDMSKLSADRGRGRTRGPRASARTQADADPGEGAKGPAA 180  
QY 154 SKS---SSIKNSLDFNVNEFPKSTDSLEPNCNASSGMTDEEOGLHKKQYGPS 210  
DB 154 SKS---SSIKNSLDFNVNEFPKSTDSLEPNCNASSGMTDEEOGLHKKQYGPS 210  
QY 181 ASSPRSDVNPVGNP- - - - -GNSSSGSTGTAEE- - - - -GPS 213  
DB 181 ASSPRSDVNPVGNP- - - - -GNSSSGSTGTAEE- - - - -GPS 213  
QY 211 N 211  
DB 211 N 211  
QY 214 S 214  
DB 214 S 214

RESULT 5  
MYB\_MAIZE  
ID MYB\_MAIZE STANDARD; PRT; 340 AA.  
AC P20024;  
DT 01-FEB-1991 (rel. 17, Created)  
DT 01-FEB-1991 (rel. 17, Last sequence update)  
DT 01-OCT-1996 (rel. 34, Last annotation update)  
DE MYB-RELATED PROTEIN ZML.  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;  
OC Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89313655; PubMed=2664447;  
RA Marocco A., Wassenbach M., Becker D., Paz-Ares J., Saedler H.,  
RA Salamoni F., Rohde W.;  
RT "Multiple genes are transcribed in Hordeum vulgare and Zea mays that carry the DNA binding domain of the myb oncoproteins.";  
RT Mol. Gen. Genet. 216:183-187(1989).  
CC -1- SIMILARITY: BELONGS TO THE MYB FAMILY.  
CC PIR; S04898; S04898.  
DR HSSP; P06876; 1MBJ.  
DR MaizeDB; 69590; -;  
DR InterPro; IPR001005; MYB\_DNA\_bind.  
DR Pfam; PF00249; myb\_DNA-binding; 2.  
DR SMART; SM00395; SANT; 2.  
DR PROSITE; PS00037; MYB\_1; 1.  
DR PROSITE; PS00334; MYB\_2; 1.



```

DR MalzeDB; 74964; -
DR InterPro; IPR001005; Myb_DNA_bind.
DR Pfam; PF00249; myb_DNA-binding; 2.
DR SMART; SM00395; SANT; 2.
DR PROSITE; PS00037; MYB_1; 1.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS50090; MYB_3; 2.
KW Nuclear protein; DNA-binding; Repeat; Transcription regulation;
KW Activator; Trans-acting factor.
FT DNA_BIND 9 MYB.
FT FT 62 102 MYB.
FT DOMAIN 203 212 POLY-GLY.
SQ SEQUENCE 252 AA; 26419 MW; AD61FA2B829C5FBD CRC64;

Query Match 27.7%; Score 439; DB 1; Length 252;
Best Local Similarity 63.5%; Pred. No. 8.8e-27;
Matches 73; Conservative 20; Mismatches 22; Indels 0; Gaps 0;

QY 1 MGSPCCERAKHTNKGTAMTKEEDRLINIRVHGEGCSMSLPRAAGILRGCKSCLRWINY 60
   ||| ||| :|||::||| | : ||| ||| :: ||| ||| ||| ||| ||| |||
Db 1 MGRBARACCAEGVARGAMTSKEDALAAVKAHGEGCKWREVPQAGLRRCGKSCLRWLNY 60
QY 61 LRPDLKRNFTTEDEIIRKLHSLGNKKSLIAGLPGRTDIEIKYNTTHRRK 115
   ||| ||| :: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 LRPNIRGRNISYDEEDLIIRHLRLLGNMWSLIAGRLPGRTEENIKYMNSTIGRR 115

RESULT 9
GLI_ARATH STANDARD; PRT; 228 AA.
ID GLI_ARATH AC P27900;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE TRICHOME DIFFERENTIATION PROTEIN GLI.
GN GLI.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92034971; Pubmed=1934056;
RA Openheimer D.G., Herman P.L., Sivakumaran S., Esch J., Marks M.D.;
RT "A myb gene required for leaf trichome differentiation in Arabidopsis
RT is expressed in stipules."
RL Cell 67:483-493(1991).
CC -1- FUNCTION: REGULATES THE PRODUCTION OF A SIGNAL THAT INDUCES
CC HAIR (TRICHOME) PRECURSOR CELLS ON LEAF PRIMORDIA TO
CC DIFFERENTIATE.
CC -1- SIMILARITY: BELONGS TO THE MYB FAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outpost.
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CC -----
DR EMBL; M79448; AAC97387.1; -
DR PIR; A39289; TYMU01.
DR HSSP; P01103; 1POM.
DR TRANSFAC; T01588; -
DR InterPro; IPR001005; Myb_DNA_bind.
DR Pfam; PF00249; myb_DNA-binding; 2.
DR SMART; SM00395; SANT; 2.
DR PROSITE; PS00037; MYB_1; 1.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS50090; MYB_3; 2.
KW Nuclear protein; DNA-binding; Repeat; Transcription regulation.
```



\*Functional antagonism between members of the myb family: B-myb  
 RT Inhibits v-myb-induced gene activation.  
 RL EMBL J. 11:4619-4629(1992).  
 RN [2]  
 RP STRUCTURE BY NMR OF 79-186.  
 RX MEDLINE-98332063; PubMed-9657674;  
 RA McInosh P.B., Frenkel T.A., Mollborn U., McCormick J.E.,  
 RT Klempner K.H., Feeney J., Carr M.D.;  
 RT Solution structure of the B-myb DNA-binding domain: a possible role  
 RT for conformational instability of the protein in DNA binding and  
 RT control of gene expression.  
 RL Biochemistry 37:9619-9629(1998).  
 CC -1- FUNCTION: IT REPRESENTS V-MYB- AND C-MYB-MEDIATED ACTIVATION OF  
 CC THE MIM-1 GENE, PROBABLY BY COMPETING WITH OTHER MYB PROTEINS  
 CC FOR BINDING SITES. IT IS AN INHIBITORY MEMBER OF THE MYB FAMILY.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEMATOPOIETIC AND NON  
 CC HEMATOPOIETIC CELLS.  
 CC -1- SIMILARITY: BELONGS TO THE MYB FAMILY.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: X67505; CAA47839.1; -  
 CC PIR: S28050; S28050.  
 CC PDB: 1A57; 01-JUL-98.  
 CC TRANSEAC: T01586; -  
 CC InterPro: IPR001005; Myb\_DNA\_bind.  
 CC Pfam: PF00249; myb-DNA-binding; 3.  
 CC SMART: SM00395; SANT; 3.  
 CC PROSITE: PS00037; MYB\_1; 3.  
 CC PROSITE: PS00034; MYB\_2; 3.  
 CC PROSITE: PS50090; MYB\_3; 3.  
 CC Transcription regulation; Nuclear protein; DNA-binding; Repeat;  
 CC 3D structure.  
 CC KW DNA\_BIND 25 77 MYB.  
 CC FT DNA\_BIND 78 129 MYB.  
 CC FT DNA\_BIND 130 180 MYB.  
 CC FT DNA\_BIND 130 180 MYB.  
 CC SEQUENCE 686 AA; 77736 MW; 2D1209EAD6489D7B CRC64;  
 SO  
 Query Match 19.7%; Score 312; DB 1; Length 686;  
 Best Local Similarity 38.6%; Pred. No. 1.6e-16;  
 Matches 64; Conservative 33; Mismatches 59; Indels 10; Gaps 3;  
 QY 14 KGAWTKEDDOLINIRVHGGCWRSLPK--AAGLLRCGKSCRLRWNYLRPDLKRGNTFTE 72  
 DB 83 KGPWTKEDDQVIELVHKYGRKQWTLIAKHLKG--RLGKQCRERHWHNLNPEYKSSWTE 140  
 QY 73 EDEDLIKLHSLGKNSLISLAGRLPGRTDNEIKRWYTHIRKRLISRGIDPQTHRPINQ 132  
 DB 141 EEDRIITSAHKGNSLISLAGRLPGRTDNEIKRWYTHIRKRLISRGIDPQTHRPINQ 132  
 QY 133 ANNTNTVTAPELDFRNS--PTSVKSSSIKNSLDFNVEFOKSTDLSEBN 178  
 DB 194 KESQPLVLLVEVDNDSQSGTRAESQTIIVNMPVDISEIKEDVDSD 239  
 RESULT 12  
 ID MYB\_XENLA STANDARD; PRT: 728 AA.  
 AC 005935;  
 DT 01-OCT-1996 (Rel. 34, Created).  
 DT 01-OCT-1996 (Rel. 34, Last sequence update).  
 DT 01-OCT-1996 (Rel. 34, Last annotation update).  
 DE MYB-RELATED PROTEIN A (A-MYB) (XMYB) (MYB-RELATED PROTEIN 2) (XMYB2).  
 GN MYB1 OR AMYB OR MYB2.  
 OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 CC Xenopodidae; Xenopus.  
 CC NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-93284408; PubMed-8510936;  
 RA Sleeman J.P.;  
 RT "Xenopus A-myb is expressed during early spermatogenesis."  
 RL Oncogene 8:1931-1941(1993).  
 RN [2]  
 RP SEQUENCE OF 1-181 FROM N.A.  
 RX MEDLINE-92297434; PubMed-1606020;  
 RA Bouwmeester T., Guenham S., El-Baradi T., Kalkbrenner F.,  
 RA van Wijk I., Moelling K., Pieler T.;  
 RT "Molecular cloning, expression and in vitro functional  
 RT characterization of Myb-related proteins in Xenopus."  
 RL Mech. Dev. 37:57-68(1992).  
 CC -1- FUNCTION: STRONG TRANSCRIPTIONAL ACTIVATOR; DNA-BINDING PROTEIN  
 CC THAT SPECIFICALLY RECOGNIZE THE SEQUENCE 5'-YAC(G/T)G-3'. COULD  
 CC HAVE A ROLE IN THE PROLIFERATION AND/OR DIFFERENTIATION OF  
 CC NEUROGENIC, SPERMATOGENIC AND B-LYMPHOID CELLS (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING EARLY SPERMATOGENESIS.  
 CC -1- SIMILARITY: BELONGS TO THE MYB FAMILY.  
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 CC  
 CC EMBL: X72620; CAA51196.1; -  
 CC EMBL: M75871; AAA49904.1; -  
 CC DR HSPF; P06876; 1MBJ.  
 CC InterPro: IPR001005; Myb\_DNA\_bind.  
 CC Pfam: PF00249; myb-DNA-binding; 3.  
 CC SMART: SM00395; SANT; 3.  
 CC PROSITE: PS00037; MYB\_1; 3.  
 CC PROSITE: PS00034; MYB\_2; 2.  
 CC PROSITE: PS50090; MYB\_3; 3.  
 CC Transcription regulation; Activator; Nuclear protein; DNA-binding;  
 CC Repeat.  
 CC KW DNA\_BIND 29 80 MYB.  
 CC FT DNA\_BIND 81 132 MYB.  
 CC FT DNA\_BIND 133 183 MYB.  
 CC FT DNA\_BIND 133 183 MYB.  
 CC FT DNA\_BIND 230 293 MYB.  
 CC FT DNA\_BIND 230 293 MYB.  
 CC FT DNA\_BIND 230 293 MYB.  
 CC SEQUENCE 728 AA; 83576 MW; 7A360CBA51AC0797 CRC64;  
 SO  
 Query Match 19.5%; Score 309; DB 1; Length 728;  
 Best Local Similarity 29.0%; Pred. No. 2.9e-15;  
 Matches 83; Conservative 45; Mismatches 96; Indels 62; Gaps 10;  
 QY 14 KGAWTKEDDOLINIRVHGGCWRSLPK--AAGLLRCGKSCRLRWNYLRPDLKRGNTFTE 72  
 DB 86 KGPWTKEDDQVIELVHKYGRKQWTLIAKHLKG--RLGKQCRERHWHNLNPEYKSSWTE 143  
 QY 73 EDEDLIKLHSLGKNSLISLAGRLPGRTDNEIKRWYTHIRKRLISRGIDPQTHRPINQ 129  
 DB 144 EEDRIITSAHKGNSLISLAGRLPGRTDNEIKRWYTHIRKRLISRGIDPQTHRPINQ 129  
 QY 130 NQANTNTVTAPELDFRNS--PTSVKSSSIKNSLDFNVEFOKSTDLSEBN 184  
 DB 204 KQA--KSCAAPNHLAQNQFYIPVQTIPIRYSSLSHD-----NCILQNSFSFIQDPF 256  
 QY 185 CASSGNTDEQOQLHKKQOYGPNSGODINIELSIGIVASDSSRVNSAASKPKVD 244

DB 257 VDA-----DDPEKERRIK-----ELLELLSAENE----- 281

OY 245 NNNFOLEQAMVAKAVCLCWLQGTSEICRNCN---SNSNGFYS 287

DB 282 -----VRRKRVPSSSLTMSSESYHMGESMNTMSHLEQCHDFYS 321

RESULT 13

MYB\_XENLA STANDARD: PRT: 743 AA.

AC P52551:

DT 01-OCT-1996 (rel. 34, Created)

DT 30-MAY-2000 (rel. 39, Last sequence update)

DT 30-MAY-2000 (rel. 39, Last annotation update)

DE MYB-RELATED PROTEIN B (B-MYB) (MYB-RELATED PROTEIN 1) (XMYB1).

GN MYB12 OR BMYB OR MYB1.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

OC Xenopodidae; Xenopus.

OX NCBI\_TaxID=83355;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92297434; PubMed=1606020;

RA Bouwmeester T., Guemann S., El-Baradi T., Kalkbrenner F.,

RA van Wijk I., Moelling K., Pieler T.;

RT "Molecular cloning, expression and in vitro functional

RT characterization of Myb-related proteins in Xenopus.";

RL Mech. Dev. 37:57-68(1992).

RN [2]

RP REVISIONS TO C-TERMINUS.

RA Humbert-Lian G., Pieler T.;

RT "Regulation of DNA-binding activity and nuclear transport of B-Myb in

RT Xenopus oocytes".

RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: NUCLEAR.

CC -1- DEVELOPMENTAL STAGE: PRESENT THROUGHOUT OOGENESIS AND EARLY

CC XENOPUS EMBRYOGENESIS; IN ADULT TISSUE IT IS PRIMARILY DETECTED IN

CC BLOOD.

CC -1- SIMILARITY: BELONGS TO THE MYB FAMILY.

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CC -----

DR EMBL; M75870; AAC98701.1; -

DR HSSP; Q03237; IASJ.

DR InterPro: IPR001005; Myb\_DNA\_bind.

DR Pfam; PF00249; myb\_DNA\_binding; 3.

DR SMART; SM00395; SANT; 3.

DR PROSITE; PS00037; MYB\_1; 3.

DR PROSITE; PS00334; MYB\_2; 3.

DR PROSITE; PS50090; MYB\_3; 3.

KW Transcription regulation; Nuclear protein; DNA-binding; Repeat.

FT DNA\_BIND 25 77 MYB.

FT DNA\_BIND 78 129 MYB.

FT DNA\_BIND 130 180 MYB.

SO SEQUENCE 743 AA; 82909 MW; 5FD1D678BB24409B CRC64;

Query Match 19 38; Score 306.5; DB 1; Length 743;

Best Local Similarity 30.88; Pred. No. 4.6e-16;

Matches 80; Conservative 37; Mismatches 56; Indels 87; Gaps 9;

OY 14 KGAWTKEDQRLNLYIVHSGEGRSLPK-AAGLLRCGSKRLRWINYLPDLKGNFTE 72

DB 83 KGPWTKEDBEKVEIVKYGKTKHTLAKQLRG--RMGKQGRERHNNHNPVKSSWTE 140

OY 73 EDELLIKLHSLGKWSLTAGRLPGRTDNEIKRWNTHTIRKLISRG1----- 121

DB 141 EEDRIIOAHNVILGNRMALIKLLPGRDNAVKNHNSITKRKVEGGLTVAKSGOEE 200

OY 122 -----DPQTH-----RPLNQTANTNTVTAPELDFRNSPTSVKSSIRKNSLDFNY 168

DB 201 REDSGYQAEEQNIVLSEPERSAN-----IPEE-----PSNLSPKL----- 239

OY 169 NEFOKSNSTDSLEBPNCYASSGMDTEQEQQLHKKQOYGPSNGODINLELSIGVNSADS 228

DB 240 -----LTKSPQIRSEOE-----SGEGSNSSEATAYV----- 266

OY 229 SRVSNANSAESKPKVDNNNF 248

DB 267 -----DSAPKRMVEYVNF 280

RESULT 14

MYB\_MOUSE STANDARD: PRT: 704 AA.

ID MYB\_MOUSE

AC P48972;

DT 01-FEB-1996 (rel. 33, Created)

DT 01-FEB-1996 (rel. 33, Last sequence update)

DT 20-AUG-2001 (rel. 40, Last annotation update)

DE MYB-RELATED PROTEIN B (B-MYB).

GN MYB12 OR BMYB.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92366176; PubMed=1501895;

RA Lam E.W., Robinson C., Watson R.J.;

RT "Characterization and cell cycle-regulated expression of mouse

RT B-myb.";

RL Oncogene 7:1885-1890(1992).

RN [2]

RP SEQUENCE OF 1-6 FROM N.A.

RX MEDLINE=93327760; PubMed=8334989;

RA Lam E.W., Watson R.J.;

RT "An E2F-binding site mediates cell-cycle regulated repression of

RT mouse B-myb transcription.";

RL EMBO J. 12:2705-2713(1993).

CC -1- SUBCELLULAR LOCATION: NUCLEAR.

CC -1- PTM: PHOSPHORYLATED BY CYCLIN A/CDK2 DURING S-PHASE.

CC PHOSPHORYLATION AT THR-524 IS PROBABLY INVOLVED IN TRANSCRIPTIONAL

CC ACTIVITY (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE MYB FAMILY.

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CC -----

DR EMBL; X70472; CAA49898.1; -

DR EMBL; X73028; CAA51511.1; -

DR HSSP; Q03237; IASJ.

DR MGD; MGI:101785; MYB12.

DR InterPro: IPR001005; Myb\_DNA\_bind.

DR Pfam; PF00249; myb\_DNA\_binding; 3.

DR SMART; SM00395; SANT; 3.

DR PROSITE; PS00037; MYB\_1; 3.

DR PROSITE; PS00334; MYB\_2; 3.

DR PROSITE; PS50090; MYB\_3; 3.

KW Transcription regulation; Nuclear protein; DNA-binding; Repeat;

KW Phosphorylation.

FT DNA\_BIND 25 77 MYB.

FT DNA\_BIND 78 129 MYB.

FT DNA\_BIND 130 180 MYB.

FT MOD\_RES 443 443 PHOSPHORYLATION (BY CDK2) (BY

RX	MEDLINE=89098307; PubMed=3145493.
RA	Urbanek P., Dvorak P., Bartunek M., Vlach P., Pecenkova J.,
RA	Paces V., Travnicek M.;
RT	"Nucleotide sequence of chicken myb proto-oncogene promoter region:
RT	detection of an evolutionarily conserved element.";
RL	Nucleic Acids Res. 16:11521-11530(1988).
RN	[4]
RP	SEQUENCE OF 73-79 FROM N.A.
RC	TISSUE=Thymus;
RX	MEDLINE=88211864; PubMed=2452755;
RA	Sorel J., Vellard M., Martinerie C., Perbal B.;
RT	"Organization of 5'-proximal c-myb exons in chicken DNA. Implications
RT	for c-myd tissue-specific transcription.";
RL	FEBS Lett. 232:227-234(1988).
RN	[5]
RP	TRUNCATION MUTATIONS.
RX	MEDLINE=91304390; PubMed=2072904;
RA	Graesser F.A., Graf T., Lipsick J.S.;
RT	"Protein truncation is required for the activation of the c-myb
RT	proto-oncogene.";
RL	Mol. Cell. Biol. 11:3987-3996(1991).
RN	[6]
RP	3D-STRUCTURE MODELING OF 142-192.
RX	MEDLINE=92285330; PubMed=1817253.
RA	Frampton J., Gibson T.J., Ness S.A., Doederlein G., Graf T.;
RT	"Proposed structure for the DNA-binding domain of the Myb oncoprotein
RT	based on model building and mutational analysis.";
RL	Protein Eng. 4:891-901(1991).
CC	-I- FUNCTION: TRANSCRIPTIONAL ACTIVATOR; DNA-BINDING PROTEIN THAT
CC	SPECIFICALLY RECOGNIZE THE SEQUENCE 5'-TAAC(G/T)G-3'. PLAYS AN
CC	IMPORTANT ROLE IN THE CONTROL OF PROLIFERATION AND DIFFERENTIATION
CC	OF HEMATOPOIETIC PROGENITOR CELLS.
CC	-I- DOMAIN: COMPRISED OF 3 DOMAINS: AN N-TERMINAL DNA-BINDING DOMAIN,
CC	A CENTRALLY LOCATED TRANSCRIPTIONAL ACTIVATION DOMAIN AND A C-
CC	TERMINAL DOMAIN INVOLVED IN TRANSCRIPTIONAL REGRESSION.
CC	-I- DOMAIN: TRUNCATION OF EITHER THE N- OR C-TERMINAL OF C-MYB LEADS
CC	TO INCREASED TRANSFORMATION AND TRANSACTIVATION POTENTIAL.
CC	-I- SIMILARITY: BELONGS TO THE MYB FAMILY.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC	-----
CC	EMBL; X03477; CAA27197.1; ALT_SEQ.
DR	EMBL; M14129; AAAA8962.1; -
DR	EMBL; X12495; CAA31015.1; -
DR	EMBL; M35509; AAAA8698.1; -
DR	EMBL; M35506; AAAA8698.1; JOINED.
DR	EMBL; M35507; AAAA8698.1; JOINED.
DR	EMBL; M35508; AAAA8698.1; JOINED.
DR	PIR; A25075; TVCHM.
DR	PDB; IPOM; 3I-OCT-93.
DR	TRANSFAC; T00139; -
DR	InterPro; IPR001005; Myb_DNA_bind.
DR	Pfam; PF00249; myd_DNA-binding; 3.
DR	SMART; SM00395; SANT; 3.
DR	PROSITE; PS00037; MYB_1; 3.
DR	PROSITE; PS00334; MYB_2; 3.
DR	PROSITE; PSS0090; MYB_3; 3.
FM	Proto-oncogene; Nuclear protein; DNA-binding; Repeat; 3D-structure.
KW	DNA_BIND 34 MYB.
FT	DNA_BIND 87 MYB.
FT	DNA_BIND 139 MYB.
FT	DNA_BIND 139 189 MYB.
FT	DOMAIN 275 327 TRANSCRIPTIONAL ACTIVATION DOMAIN
FT	DOMAIN 328 465 (BY SIMILARITY)
FT	DOMAIN 376 397 NEGATIVE REGULATORY DOMAIN (BY
FT	DOMAIN 376 397 SIMILARITY).
FT	LEUCINE-ZIPPER.





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OM protein - protein search, using sw model

Run on: January 23, 2002, 21:11:38 ; Search time 91.99 Seconds

(Without alignments)  
467.486 Million cell updates/sec

Title: US-09-453-387A-2  
Perfect score: 1584  
Sequence: 1 MGRSPCCERAHNTKAWTEKE.....RNCNSNSNGFYSCRPIDS 294

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues  
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SP:REMBL\_17:\*  
2: sp.archaea:\*  
3: sp.bacteria:\*  
4: sp.fungi:\*  
5: sp.human:\*  
6: sp.invertebrate:\*  
7: sp.mammal:\*  
8: sp.mhc:\*  
9: sp.organelle:\*  
10: sp.plant:\*  
11: sp.priant:\*  
12: sp.virus:\*  
13: sp.vertebrate:\*  
14: sp.unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1584	100.0	294	10	Q43436 gossypium h
2	854.5	53.9	274	10	P81395 arabidopsis h
3	768	48.5	257	10	Q959K9 arabidopsis
4	762	48.1	236	10	Q38851 arabidopsis
5	756.5	47.8	251	10	Q06944 hordeum vul
6	728	46.0	273	10	Q43525 lycopersico
7	726	45.8	264	10	Q9ATD1 gossypium h
8	723	45.6	282	10	Q9SZP1 arabidopsis
9	717	45.3	282	10	Q49774 arabidopsis
10	704.5	44.5	232	10	P81393 arabidopsis
11	702	44.3	246	10	Q9S7Y2 arabidopsis
12	684	43.2	274	10	Q9SMZ8 arabidopsis
13	684	43.2	274	10	Q43608 arabidopsis
14	683	43.1	239	10	Q23889 oryza sativ
15	681.5	43.0	269	10	Q42379 arabidopsis
16	674.5	42.6	212	10	Q9SDS8 arabidopsis
17	652	41.2	276	10	Q23890 oryza sativ
18	626.5	39.6	226	10	Q49021 gossypium h
19	584.5	36.9	321	10	Q9LIDS arabidopsis

20	584.5	36.9	352	10	Q9LDE2	Q91fe2 arabidopsis
21	567	35.8	325	10 <td>Q9LEF1</td> <td>Q91fe1 arabidopsis</td>	Q9LEF1	Q91fe1 arabidopsis
22	553.5	34.9	345	10 <td>Q9LE63</td> <td>Q91e63 arabidopsis</td>	Q9LE63	Q91e63 arabidopsis
23	549.5	34.7	282	10 <td>Q9M0J5</td> <td>Q9m0j5 arabidopsis</td>	Q9M0J5	Q9m0j5 arabidopsis
24	546.5	34.5	274	10 <td>Q40173</td> <td>Q40173 lycopersico</td>	Q40173	Q40173 lycopersico
25	546	34.5	247	10 <td>Q9ATD9</td> <td>Q9atd9 gossypium h</td>	Q9ATD9	Q9atd9 gossypium h
26	543	34.3	414	10 <td>Q9SAV9</td> <td>Q9sav9 arabidopsis</td>	Q9SAV9	Q9sav9 arabidopsis
27	539.5	34.1	254	10 <td>Q9ATD2</td> <td>Q9atd2 gossypium h</td>	Q9ATD2	Q9atd2 gossypium h
28	539.5	34.0	350	10 <td>Q9LDR8</td> <td>Q9ldr8 arabidopsis</td>	Q9LDR8	Q9ldr8 arabidopsis
29	539	34.0	352	10	Q22685	Q22685 arabidopsis
30	537	33.9	368	10 <td>Q04141</td> <td>Q04141 oryza sativ</td>	Q04141	Q04141 oryza sativ
31	536	33.8	388	10 <td>Q40920</td> <td>Q40920 picea maria</td>	Q40920	Q40920 picea maria
32	534.5	33.7	324	10 <td>Q9M0Y5</td> <td>Q9m0y5 arabidopsis</td>	Q9M0Y5	Q9m0y5 arabidopsis
33	533.5	33.6	326	10 <td>Q9LXFL</td> <td>Q9lxf1 arabidopsis</td>	Q9LXFL	Q9lxf1 arabidopsis
34	531.5	33.6	286	10 <td>Q9SPG1</td> <td>Q9spg1 arabidopsis</td>	Q9SPG1	Q9spg1 arabidopsis
35	531	33.5	327	10 <td>Q9SPG7</td> <td>Q9spg7 arabidopsis</td>	Q9SPG7	Q9spg7 arabidopsis
36	530.5	33.5	269	10 <td>Q9SE64</td> <td>Q9sec4 plumbella</td>	Q9SE64	Q9sec4 plumbella
37	530	33.5	282	10 <td>Q9CTU7</td> <td>Q9ctu7 arabidopsis</td>	Q9CTU7	Q9ctu7 arabidopsis
38	528.5	33.4	352	10 <td>Q65409</td> <td>Q65409 arabidopsis</td>	Q65409	Q65409 arabidopsis
39	528	33.3	421	10 <td>Q02992</td> <td>Q02992 petunia hyb</td>	Q02992	Q02992 petunia hyb
40	526	33.2	314	10 <td>Q9C695</td> <td>Q9c695 arabidopsis</td>	Q9C695	Q9c695 arabidopsis
41	526	33.2	578	10 <td>Q9FVU6</td> <td>Q9fvu6 arabidopsis</td>	Q9FVU6	Q9fvu6 arabidopsis
42	524.5	33.1	340	10 <td>Q9FR07</td> <td>Q9fr07 zea mays su</td>	Q9FR07	Q9fr07 zea mays su
43	524	33.1	249	10 <td>Q38850</td> <td>Q38850 arabidopsis</td>	Q38850	Q38850 arabidopsis
44	523.5	33.0	336	10 <td>Q9FLR1</td> <td>Q9flr1 arabidopsis</td>	Q9FLR1	Q9flr1 arabidopsis
45	522	33.0	299	10 <td>Q9M2D9</td> <td>Q9m2d9 arabidopsis</td>	Q9M2D9	Q9m2d9 arabidopsis

## ALIGNMENTS

## RESULT 1

ID Q43436 PRELIMINARY: PRT: 294 AA.

AC Q43436;  
DT 01-NOV-1996 (TRENBLREL. 01, Created)  
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
DT 01-JUN-2001 (TRENBLREL. 17, Last annotation update)  
DE COTTON DNA-BINDING DOMAIN MRNA.  
GN MYB.  
OS Gossypium hirsutum (Upland cotton).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot; Rosidae;  
OC eurosids II; Malvales; Malvaceae; Gossypium.  
OX NCBI\_TaxID=3635;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. ACALA SJ-2; TISSUE=OVULE;  
RA Walkins T.A., Lu C.C.;  
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL; L04497; AAA33067.1;  
DR HSBP; P01103; IPOM.  
DR TRANSFAC; T02864;  
DR Mendel; 8407; Goshi.Myb.8407.  
DR InterPro; IPR001005; MYB\_DNA\_bind.  
DR Pfam; PF00249; MYB\_DNA-binding; 2.  
DR SMART; SM00395; SANT; 2.  
DR PROSITE; PS00037; MYB\_1; UNKNOWN\_1.  
DR PROSITE; PS00334; MYB\_2; 1.  
DR PROSITE; PS50090; MYB\_3; 2.  
KW DNA-binding.  
SQ SEQUENCE 294 AA; 33202 MW; EF1A55B64919F0AC CRC64;

Query Match 100.0%; Score 1584; DB 10; Length 294;

Best Local Similarity 100.0%; Pred. No. 2.2e-130; Mismatches 0; Indels 0; Gaps 0;

OY 1 MGRSPCCERAHNTKAWTEKEORLLNTFYHVGCGRSRPKAGILRCGSCRLRWNY 60  
DB 1 MGRSPCCERAHNTKAWTEKEORLLNTFYHVBGGRSLPKAAGLLRCGSCRLRWNY 60  
OY 61 LRPDLKRGNTFEDELLIKLHSLGNKWSLIAGRLPGRTDNEIKNYWTHIKRKLISRG 120

```

Db 61 LRPDLKRGNTFEEDEDELIKLSHSLGKWSLGRLEGRDNEIKYWNTHIKRKLISRG 120
Oy 121 IDPQTHRLPNOTANTNTVTAPELDFRNSPTSVSKSSIKRPSLDENFNEOFKNTDSL 180
Db 121 IDPQTHRLPNOTANTNTVTAPELDFRNSPTSVSKSSIKRPSLDENFNEOFKNTDSL 180
Oy 181 EEPNCTASSGMMTDEEQOELHKKOQYGPSPNGODINLELSIGIYSADSSRYSNANSAESK 240
Db 181 EEPNCTASSGMMTDEEQOELHKKOQYGPSPNGODINLELSIGIYSADSSRYSNANSAESK 240
Oy 241 PRVDNNNFQFLQAMAKAVCLCWLQGFSTSEICRNCNSNSNGFYSCRPIDS 294
Db 241 PRVDNNNFQFLQAMAKAVCLCWLQGFSTSEICRNCNSNSNGFYSCRPIDS 294

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## RESULT 2

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P81395 PRELIMINARY; PRT; 274 AA.
ID P81395;
AC P81395;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE MYB-RELATED PROTEIN 330.
GN MYB 330.
OS Antirrhinum majus (Garden snapdragon).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; eusteridae I; Lamiales; Veroniceae; Antirrhinum.
OX NCBI_TaxID=4151;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-J1:522; TISSUE=FLOWER BUDS;
RX MEDLINE=93005689; PubMed=1840903;
RA Jackson D., Callan-Mackay F., Prescott A.G., Roberts K., Martin C.;
RA "Expression patterns of myb genes from Antirrhinum flowers.";
RL Plant Cell 3:115-125(1991).
CC -1- FUNCTION: MAY BE A TRANSCRIPTIONAL ACTIVATOR.
CC -1- TISSUE SPECIFICITY: MATURE FLOWER.
CC -1- SIMILARITY: BELONGS TO THE MYB FAMILY OF PROTEINS.
DR PIR, J00957; J00957.
DR HSSP, P01103; IPOM.
DR TRANSFAC, T02928; -.
DR Mendel, 24823; Antma:Myb:24823.
DR InterPro: IPR001005; Myb_DNA_bind.
DR Pfam: PF00249; myb_DNA-binding; 2.
DR SMART, SM00395; SANT; 2.
DR PROSITE, PS00037; MYB_1; UNKNOWN_1.
DR PROSITE, PS00034; MYB_2; 1.
DR PROSITE, PS50090; MYB_3; 2.
KW Nuclear protein; DNA-binding; Repeat; Transcription regulation.
FT DNA_BIND 9 61 MYB.
FT DNAS_BIND 62 102 MYB.
SQ SEQUENCE 274 AA; 30679 MW; 69831BC41161BEBB CRC64;

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Query Match 53.9%; Score 854.5; DB 10; Length 274;
Best Local Similarity 60.5%; Pred. No. 8.6e-67;
Matches 178; Conservative 23; Mismatches 68; Indels 25; Gaps 8;
Oy 1 MGRSPCCAKHTNKGAMTKEDQRLINIRVHGEQWRSLEPKAAGLLRCGSKSRLRWNY 60
Db 1 MGRSPCCAKHTNKGAMTKEDQRLINIRVHGEQWRSLEPKAAGLLRCGSKSRLRWNY 60
Oy 61 LRPDLKRGNTFEEDEDELIKLSHSLGKWSLGRLEGRDNEIKYWNTHIKRKLISRG 120
Db 61 LRPDLKRGNTFEEDEDELIKLSHSLGKWSLGRLEGRDNEIKYWNTHIKRKLISRG 120
Oy 121 IDPQTHRLPNOTANTNTVTAPELDFRNSPTSVSKSSIKRPSLDENFNEOFKNTDSL 176
Db 121 IDPQTHRLPNOTANTNTVTAPELDFRNSPTSVSKSSIKRPSLDENFNEOFKNTDSL 176
Oy 121 IDPQTHRLPNOTANTNTVTAPELDFRNSPTSVSKSSIKRPSLDENFNEOFKNTDSL 170
Db 121 IDPQTHRLPNOTANTNTVTAPELDFRNSPTSVSKSSIKRPSLDENFNEOFKNTDSL 170
Oy 177 TDSLEPNCTASSGMMTDEEQOELHKKOQYGPSPNGODINLELSIGIYSADSSRYSNAN 236

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Db 171 SSSDDTKCNSS---TTEESQSLTPPKKEEKSVPLVDLSLGLPQSQCNKSVSLN 226
Oy 237 AESKPKYDNNNFQFLQAMAKAVCLCWLQGFSTSEICRNCNSNSNGFYSCRPIDS 289
Db 227 SSSSGFYD---LFRPAKVAQRCVCWKWTGLQXGDEQCNCO--SFNGFYRIC 274

```

## RESULT 3

```

O9S9K9 PRELIMINARY; PRT; 257 AA.
ID O9S9K9;
AC O9S9K9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE T22J18.19 PROTEIN.
GN T22J18.19.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Vysotskaya V.S., Schwartz J.R., Toriumi M., Yu G., Oji O., Kwan A.,
RA Liu S., Li J., Araujo R., Au M., Brendel V., Buehler E., Conway A.B.,
RA Conway A.J., Dewar K., Feng J., Kim C., Kurtz D., Li Y., Palm C.J.,
RA Shih P., Sun H., Davis R.W., Ecker J.R., Federspiel N.A.,
RA "Arabidopsis thaliana chromosome 1 BAC T22J18 sequence, complete
RT sequence.";
RT Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Theologis A.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Theologis;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL, AC003879; AAC25522.1; -.
DR HSSP, P01103; IPOM.
DR InterPro: IPR001005; Myb_DNA_bind.
DR Pfam: PF00249; myb_DNA-binding; 2.
DR SMART, SM00395; SANT; 2.
DR PROSITE, PS00037; MYB_1; UNKNOWN_1.
DR PROSITE, PS00034; MYB_2; 1.
DR PROSITE, PS50090; MYB_3; 2.
SQ SEQUENCE 257 AA; 29352 MW; 132D80DEA58D7D93 CRC64;

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Query Match 48.5%; Score 768; DB 10; Length 257;
Best Local Similarity 55.6%; Pred. No. 2.8e-59;
Matches 160; Conservative 33; Mismatches 53; Indels 42; Gaps 7;
Oy 1 MGRSPCCAKHTNKGAMTKEDQRLINIRVHGEQWRSLEPKAAGLLRCGSKSRLRWNY 60
Db 1 MGRSPCCAKHTNKGAMTKEDQRLINIRVHGEQWRSLEPKAAGLLRCGSKSRLRWNY 60
Oy 61 LRPDLKRGNTFEEDEDELIKLSHSLGKWSLGRLEGRDNEIKYWNTHIKRKLISRG 120
Db 61 LRPDLKRGNTFEEDEDELIKLSHSLGKWSLGRLEGRDNEIKYWNTHIKRKLISRG 120
Oy 121 IDPQTHRLPNOTANTNTVTAPELDFRNSPTSVSKSSIKRPSLDENFNEOFKNTDSL 180
Db 121 IDPQTHRLPNOTANTNTVTAPELDFRNSPTSVSKSSIKRPSLDENFNEOFKNTDSL 180
Oy 121 IDPQTHRLPNOTANTNTVTAPELDFRNSPTSVSKSSIKRPSLDENFNEOFKNTDSL 160
Db 121 IDPQTHRLPNOTANTNTVTAPELDFRNSPTSVSKSSIKRPSLDENFNEOFKNTDSL 160
Oy 181 EEPNCTASSGMMTDEEQOELHKKOQYGPSPNGODINLELSIGIYSADSSRYSNAN 233
Db 181 EEPNCTASSGMMTDEEQOELHKKOQYGPSPNGODINLELSIGIYSADSSRYSNAN 233
Oy 161 REISGMWNNC-ESSGTTSEKD-----YGNEDAWNLNLELSIGIYSADSSRYSTRVSV 209
Db 234 ASAESKPKYDNNNFQFLQAMAKAVCLCWLQGFSTSEICRNCNSN 281

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DB 210 VDSASTRMWSELF-----GAGESDVAVLCCLCRILGFRNESCRCRVS 253

RESULT 4

ID 038851 PRELIMINARY; PRT; 236 AA.

AC 038851; 01-NOV-1996 (TREMELREL. 01, Created)

DT 01-NOV-1996 (TREMELREL. 01, Last sequence update)

DE 01-JUN-2001 (TREMELREL. 17, Last annotation update)

DN DNA-BINDING PROTEIN.

GN MYB OR MYB2.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC Eurosidia II; Brassicales; Brassicaceae; Arabidopsi.

OX NCBI\_Taxid:3702;

RA SEQUENCE FROM N.A.

RC STRAIN-LANDSBERG ERECTA;

RA MEDLINE-96132152; PubMed-8580966;

RT L.I.S.F., Parish R.W.;

RT "Isolation of two novel myb-like genes from Arabidopsis and studies on

the DNA-binding properties of their products."

PL Plant J. 8:963-972(1995).

RA SEQUENCE FROM N.A.

RC STRAIN-LANDSBERG ERECTA;

RA Headlewood J.L.;

RT Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.

RA SEQUENCE FROM N.A.

RC STRAIN-LANDSBERG ERECTA;

RA Headlewood J.L.;

RT Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.

RA SEQUENCE FROM N.A.

RC STRAIN-LANDSBERG ERECTA;

RA Headlewood J.L.;

RT Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.

RA SEQUENCE FROM N.A.

RC STRAIN-LANDSBERG ERECTA;

RA Headlewood J.L.;

RT Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.

RA SEQUENCE FROM N.A.

RC STRAIN-LANDSBERG ERECTA;

RA Headlewood J.L.;

RT Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.

RA SEQUENCE FROM N.A.

RC STRAIN-LANDSBERG ERECTA;

RA Headlewood J.L.;

RT Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.

RA SEQUENCE FROM N.A.

RC STRAIN-LANDSBERG ERECTA;

RA Headlewood J.L.;

RT Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.

RA SEQUENCE FROM N.A.

RC STRAIN-LANDSBERG ERECTA;

RA Headlewood J.L.;

RT Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.

RA SEQUENCE FROM N.A.

RC STRAIN-LANDSBERG ERECTA;

RA Headlewood J.L.;

RT Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.

RA SEQUENCE FROM N.A.

QY 180 LEEPNCATSGMTDEEQLKROQYGPSNGQ-DINLELSIGIYASDSSRVNSANSAE 238

DB 164 SSD-NGASTSGTTDEDLNQ--NGECYSDNSGHINKMLDTLGLFGSMGRIYVGSSAD 220

QY 239 SKPKVD 244

DB 221 SKPMCD 226

RESULT 5

ID 006944 PRELIMINARY; PRT; 251 AA.

AC 006944;

DT 01-NOV-1996 (TREMELREL. 01, Created)

DT 01-NOV-1996 (TREMELREL. 01, Last sequence update)

DT 01-JUN-2001 (TREMELREL. 17, Last annotation update)

DE MYBHV5 PROTEIN.

GN HV5 OR MYB2.

OS Hordeum vulgare (Barley).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;

OC Triticeae; Hordeum.

OX NCBI\_Taxid-4513;

RA SEQUENCE FROM N.A.

RC STRAIN-CV ABYSSINIAN 2231; TISSUE-SHOOT MERISTEM;

RA MEDLINE-94035190; PubMed-8220488;

RT Wilsenbach M., Ueberlackner B., Vogt F., Becker D., Salamini F.,

RA Rohde W.;

RT "Myb genes from Hordeum vulgare: tissue-specific expression of

chimeric Myb promoter/Gus genes in transgenic tobacco."

PL Plant J. 4:411-422(1993).

RA SEQUENCE FROM N.A.

RC STRAIN-CV ABYSSINIAN 2231; TISSUE-SHOOT MERISTEM;

RA Rohde W., Morocco A., Wilsenbach M., Barzen E., Kristiansen K.,

RA Salamini F.;

RA (in) Styles D.E., Gavazzi G., Racchi M.S. (eds.);

RL The genetics of flavonoids, pp.79-95, Edizioni Edicopli,

RL Milano (1988).

DR EMBL; X70876; CA50221.1;

DR EMBL; X70880; CA50225.1;

DR HSSP; P01103; IPOM.

DR TRANSFAC; T02888;

DR Mendel; 8596; Horvu; Myb; 8596.

DR InterPro; IPR001005; Myb\_DNA\_bind.

DR Pfam; PF00249; myb\_DNA-binding; 2.

DR SMART; SM00395; SANT; 2.

DR PROSITE; PS00037; MYB\_1; UNKNOWN\_1.

DR PROSITE; PS00334; MYB\_2; 1.

DR PROSITE; PS50090; MYB\_3; 2.

KW Nuclear protein; DNA-binding; Activator; Transcription regulation;

KW Repeat.

FT DNA\_BIND 62 102 MYB.

FT DNA\_BIND 251 AA; 27602 MM; 07EL2727D3D8EB25 CRC64;

SEQUENCE

Query Match 47.8%; Score 756.5; DB 10; Length 251;

Best Local Similarity 50.7%; Pred. No. 2,7e-58;

Matches 152; Conservative 32; Mismatches 55; Indels 61; Gaps 6;

QY 1 MGRSPCCAKHTNKAMTKEDORLNTYRVHGGCWRSLPKAAGLLRCGSKRLRMNY 60

DB 1 MGRSPCCAKHTNKAMTKEDORLNTYRVHGGCWRSLPKAAGLLRCGSKRLRMNY 60

QY 61 LRPDLKRGNTFEDEELIKLSILGNKWSLTAGRLPGRTDNEIKYWNTHIRKRLISRG 120

DB 61 LRPDLKRGNTFEDEELIKLSILGNKWSLTAGRLPGRTDNEIKYWNTHIRKRLISRG 120

QY 121 IDPQTHRLPNTANTNTYAPTEL--DFRNSPTSV--SKSSSINPISLDFYNEFOFSKNT 177

DB 121 IDPQTHRLPNTANTNTYAPTEL--DFRNSPTSV--SKSSSINPISLDFYNEFOFSKNT 177

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Db 121 MDPHTHRLTAVIDAAAPTRPAQIAVAPARAAPTMTALPTKQOOPPVPESSDDGSSGA 180
QY 178 DSELPNCTASSGMTTDEOQOHLKKOQYSPNGODINLELSIGIYSANSSRVNANSA 237
Db 181 TSTGPRC-----PDLNLDLSVGPAPDAP----- 205
QY 238 ESKPVDNNNFQFLBOAMVAKAVCLCMOLGFGTSEICRNCONSN-----NGFYSYCRPLD 293
Db 206 -----TSHPYCLCRHLGFRGEGAC-SCROADSASQSGGFRFRLE 246

RESULT 6
043525 PRELIMINARY; PRT; 273 AA.
AC 043525
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE TRANSCRIPTION FACTOR.
GN MYB OR THM27.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ALISA CRAIG; TISSUE=HYPOCOTYL;
RX MEDLINE=96270378; PubMed=8639738;
RA Llan O., Hamilton W.D.O., Merryweather A.;
RT Cloning and initial characterization of 14 myb-related cDNAs from
RT tomato (Lycopersicon esculentum cv. Alisa Craig).";
RL Plant Mol. Biol. 30:1009-1020(1996).
DR EMBL; X95296; CAA64614.1;
DR HSSP; P01103; IPOM.
DR TRANSFAC; T02886;
DR Mendel; 8912; Lycos; myb.8912.
DR InterPro; IPR001005; myb_DNA_bind.
DR Pfam; PF00249; myb_DNA-binding; 2.
DR SMART; SM00395; SANT; 2.
DR PROSITE; PS00037; MYB_1; 1.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS00090; MYB_3; 2.
SQ SEQUENCE 273 AA; 31100 MW; 6F2E9365F3003AFB CRC64;

Query Match
Best Local Similarity 53.0%; Score 728; DB 10; Length 273;
Matches 151; Conservative 26; Mismatches 64; Indels 44; Gaps 5;

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ID 09ATD1 PRELIMINARY; PRT; 264 AA.
AC 09ATD1;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE GHMYB9.
GN GHMYB9.
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euosids II; Malvales; Malvaceae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ACALA MAXXA; TISSUE=DAY OF ANTHESIS OVULE;
RA Matz E.C., Burr B.;
RT "Cotton seed fibers are trichomes.";
RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF336286; AAK19619.1;
SQ SEQUENCE 264 AA; 29629 MW; E09BCEBAE7662E95 CRC64;

Query Match
Best Local Similarity 45.8%; Score 726; DB 10; Length 264;
Matches 153; Conservative 27; Mismatches 53; Indels 68; Gaps 7;

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QY 1 MGRSPCCERAKHTNGAMTKEDORLNIYIRVHGCGCRSLPKAAGLRCCKSRLRWINY 60
Db 1 MGRSPCCERAKHTNGAMTKEDORLNIYIRVHGCGCRSLPKAAGLRCCKSRLRWINY 60
QY 61 LRPLDKGNFTEEBDELIIKLSLGNKWSLAGRLPGRTDNEIKYWNTHIRKLLISRG 120
Db 61 LRPLDKGNFTEEBDELIIKLSLGNKWSLAGRLPGRTDNEIKYWNTHIRKLLISRG 120
QY 121 IDPQTHRLPLNOTANTNTVTAPELDFRNSPTSVSKSSSIKNPSLDFNYNEFOFKSWTDSL 180
Db 121 IDPQTHRLPLNOTANTNTVTAPELDFRNSPTSVSKSSSIKNPSLDFNYNEFOFKSWTDSL 180
QY 121 IDPQTHRLPLNOTANTNTVTAPELDFRNSPTSVSKSSSIKNPSLDFNYNEFOFKSWTDSL 180
Db 121 IDPQTHRLPLNOTANTNTVTAPELDFRNSPTSVSKSSSIKNPSLDFNYNEFOFKSWTDSL 180
QY 181 EEPNCTASSGMTTDEOQOHLKKOQYSPNGODINLELSIGIYSANSSRVNANSAESK 240
Db 181 EEPNCTASSGMTTDEOQOHLKKOQYSPNGODINLELSIGIYSANSSRVNANSAESK 240
QY 158 EMINIAAEFVETSKESDNNEI--IOEKSSSCLPDLNLELRI-----SPHH 201
Db 158 EMINIAAEFVETSKESDNNEI--IOEKSSSCLPDLNLELRI-----SPHH 201
QY 241 PKVDNNNFQFLBOAMVAKAVCLCMOLGFGTSEICRNCONSNNGF 285
Db 202 QOQDHRHHH-----QNSSSLCFTCSLGIQNSKDCSGSSSNGNGW 241

RESULT 7
09ATD1

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QY 1 MGRSPCCERAKHTNGAMTKEDORLNIYIRVHGCGCRSLPKAAGLRCCKSRLRWINY 60
Db 1 MGRSPCCERAKHTNGAMTKEDORLNIYIRVHGCGCRSLPKAAGLRCCKSRLRWINY 60
QY 61 LRPLDKGNFTEEBDELIIKLSLGNKWSLAGRLPGRTDNEIKYWNTHIRKLLISRG 120
Db 61 LRPLDKGNFTEEBDELIIKLSLGNKWSLAGRLPGRTDNEIKYWNTHIRKLLISRG 120
QY 121 IDPQTHRLPLNOTANTNTVTAPELDFRNSPTSVSKSSSIKNPSLDFNYNEFOFKSWTDSL 180
Db 121 IDPQTHRLPLNOTANTNTVTAPELDFRNSPTSVSKSSSIKNPSLDFNYNEFOFKSWTDSL 180
QY 121 IDPQTHRLPLNOTANTNTVTAPELDFRNSPTSVSKSSSIKNPSLDFNYNEFOFKSWTDSL 180
Db 121 IDPQTHRLPLNOTANTNTVTAPELDFRNSPTSVSKSSSIKNPSLDFNYNEFOFKSWTDSL 180
QY 181 EEPNCTASSGMTTDEOQOHLKKOQYSPNGODINLELSIGIYSANSSRVNANSAESK 240
Db 181 EEPNCTASSGMTTDEOQOHLKKOQYSPNGODINLELSIGIYSANSSRVNANSAESK 240
QY 157 NNP-----IGFTTDEKRIPOVER-----CPDLNLDL-----RISPYIOQTO 194
Db 157 NNP-----IGFTTDEKRIPOVER-----CPDLNLDL-----RISPYIOQTO 194
QY 241 PKVDNNNFQFLBOAMVAKAVCLCMOLGFGTSEICRNCONSNNGFYS 287
Db 195 PESFKTG-----GRTLCITCSLGVKNKDCSTITTAAGSSSSSSSHSNSSG 245

QY 288 Y 288
Db 246 Y 246

RESULT 8
09ATD1 PRELIMINARY; PRT; 282 AA.
ID 09ATD1;
AC 09ATD1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE PUTATIVE TRANSCRIPTION FACTOR (MYB4).
GN F20M13.180 OR AT4G38620.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Kutzn M., Wambutt R., Bancroft I., Mewes H.W.,
RA Beyer M., Wedler H., Schueller C.;
RA Mayer K.F.X., Schueller C.;
RL Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;

```

RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Murphy G., Ridley P., Hudson S., Mewes H.W., Lemcke K., Mayer K.F.X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL035540; CAB37518.1; -  
 DR EMBL: AL161593; CAB80526.1; -  
 DR HSSP: P01103; 1POM.  
 DR InterPro: IPR001005; MYB\_DNA\_bind.  
 DR Pfam: PF00249; MYB\_DNA-binding; 2.  
 DR SMART: SM00395; SANT; 2.  
 DR PROSITE: PS00037; MYB\_1; 1.  
 DR PROSITE: PS00334; MYB\_2; 1.  
 DR PROSITE: PS50090; MYB\_3; 2.  
 DR PROSITE: PS50090; MYB\_3; 2.  
 SQ SEQUENCE 282 AA; 31808 MW; CEFBAFIE9DBA8687 CRC64;

Query Match 45.6%; Score 723; DB 10; Length 282;  
 Best Local Similarity 52.0%; Pred. No. 2.6e-55;  
 Matches 146; Conservative 38; Mismatches 49; Indels 48; Gaps 7;

QY 1 MGRSPCEKATNKGAATKEEDORLINTYRVHGGCGMRSIPKAGLLRCGKSCRLRWNY 60  
 DB 1 MGRSPCEKATNKGAATKEEDORLINTYRVHGGCGMRSIPKAGLLRCGKSCRLRWNY 60  
 QY 61 LRPDLKRGNTFEEDDELIIKLSLLGNKWSLIAGRLPGRTDNEIKYWNTHIRKRLISRG 120  
 DB 61 LRPDLKRGNTFEEDDELIIKLSLLGNKWSLIAGRLPGRTDNEIKYWNTHIRKRLISRG 120  
 QY 121 IDPOTHRPLNQTANTNTYAPTELDPRNSPT-SYSSSSSTKNSLDENYNEQFQKSTMS 179  
 DB 121 IDPOTHRPLNQTANTNTYAPTELDPRNSPT-SYSSSSSTKNSLDENYNEQFQKSTMS 179  
 QY 121 IDPOTHRPLNQTANTNTYAPTELDPRNSPT-SYSSSSSTKNSLDENYNEQFQKSTMS 176  
 DB 121 IDPOTHRPLNQTANTNTYAPTELDPRNSPT-SYSSSSSTKNSLDENYNEQFQKSTMS 176  
 QY 180 LEPNCTASGCTDEEOQLHKKOQYGPNSGODINLEL----- 219  
 DB 177 I-----SMLETRKEEDCEPVQEK-----PDNLLELRISLPDDVDRLQHGKSTTP 222  
 QY 220 -----SIGIVSADSSRVSNAN-----SAESKPKVDNNNFQFL 251  
 DB 223 RCFKCSLGMINGMECRGMRCDYVGSSKSGSDMSNGDFL 263

RESULT 9  
 ID 049774 PRELIMINARY; PRT; 282 AA.  
 AC 049774;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1999 (TREMBLrel. 11, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE PUTATIVE TRANSCRIPTION FACTOR (R2R3-MYB TRANSCRIPTION FACTOR).  
 GN MYB4.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. COLUMBIA;  
 RX MEDLINE-99056848; PubMed-9839469;  
 RA Kitzan H.D., Denekamp M., Greco R., Jin H.-L., Leyva A., Weissner R.,  
 RA Petroni K., Uzaliqui A., Bevan M., Martin C., Smeekens S.,  
 RA Tonelli C., Paz-Ares J., Weishaar B.;  
 RT "Towards functional characterisation of the members of the R2R3-MYB  
 gene family from Arabidopsis thaliana.";  
 RL Plant J. 16:263-276(1998).  
 RN [2]  
 RP SEQUENCE OF 55-99 FROM N.A.  
 RC TISSUE-WHOLE PLANTS;

RA Romero I., Fuentes A., Benito M.J., Malpica J., Leyva A., Paz-Ares J.;  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF062860; AAC3582.1; -  
 DR EMBL: Z95763; CAB09195.1; -  
 DR HSSP: P01103; 1POM.  
 DR Mendel: 27725; Arabn; MYB; 27725.  
 DR InterPro: IPR001005; MYB\_DNA\_bind.  
 DR Pfam: PF00249; MYB\_DNA-binding; 2.  
 DR SMART: SM00395; SANT; 2.  
 DR PROSITE: PS00037; MYB\_1; 1.  
 DR PROSITE: PS00334; MYB\_2; 1.  
 DR PROSITE: PS50090; MYB\_3; 4.  
 DR PROSITE: PS50090; MYB\_3; 4.  
 SQ SEQUENCE 282 AA; 31820 MW; F4CB4F0B47B575AD CRC64;

Query Match 45.3%; Score 717; DB 10; Length 282;  
 Best Local Similarity 51.6%; Pred. No. 8.7e-55;  
 Matches 145; Conservative 38; Mismatches 50; Indels 48; Gaps 7;

QY 1 MGRSPCEKATNKGAATKEEDORLINTYRVHGGCGMRSIPKAGLLRCGKSCRLRWNY 60  
 DB 1 MGRSPCEKATNKGAATKEEDORLINTYRVHGGCGMRSIPKAGLLRCGKSCRLRWNY 60  
 QY 61 LRPDLKRGNTFEEDDELIIKLSLLGNKWSLIAGRLPGRTDNEIKYWNTHIRKRLISRG 120  
 DB 61 LRPDLKRGNTFEEDDELIIKLSLLGNKWSLIAGRLPGRTDNEIKYWNTHIRKRLISRG 120  
 QY 121 IDPOTHRPLNQTANTNTYAPTELDPRNSPT-SYSSSSSTKNSLDENYNEQFQKSTMS 179  
 DB 121 IDPOTHRPLNQTANTNTYAPTELDPRNSPT-SYSSSSSTKNSLDENYNEQFQKSTMS 179  
 QY 121 IDPOTHRPLNQTANTNTYAPTELDPRNSPT-SYSSSSSTKNSLDENYNEQFQKSTMS 176  
 DB 121 IDPOTHRPLNQTANTNTYAPTELDPRNSPT-SYSSSSSTKNSLDENYNEQFQKSTMS 176  
 QY 180 LEPNCTASGCTDEEOQLHKKOQYGPNSGODINLEL----- 219  
 DB 177 I-----SMLETRKEEDCEPVQEK-----PDNLLELRISLPDDVDRLQHGKSTTP 222  
 QY 220 -----SIGIVSADSSRVSNAN-----SAESKPKVDNNNFQFL 251  
 DB 223 RCFKCSLGMINGMECRGMRCDYVGSSKSGSDMSNGDFL 263

RESULT 10  
 ID P81393 PRELIMINARY; PRT; 232 AA.  
 AC P81393;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE MYB-RELATED PROTEIN 308.  
 GN MYB 308.  
 OS Antirrhinum majus (Garden snapdragon).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Lamiales; Veroniceae; Antirrhinum.  
 OC NCBI\_TaxID=4151;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-JT:522; TISSUE-FLOWER BUDS;  
 RX MEDLINE-93005689; PubMed-1840903;  
 RA Jackson D., Cullanez-Macia F., Prescott A.G., Roberts K., Martin C.;  
 RT "Expression patterns of myb genes from Antirrhinum flowers.";  
 RL Plant Cell 3:115-125(1991).  
 CC -1- FUNCTION: MAY BE A TRANSCRIPTIONAL ACTIVATOR.  
 CC -1- TISSUE SPECIFICITY: ROOT, STEM, LEAF, SEED POD, IMMATURE FLOWER  
 AND MATURE FLOWER.  
 CC -1- SIMILARITY: BELONGS TO THE MYB FAMILY OF PROTEINS.  
 CC PIR: J00960; J00960.  
 DR HSSP: P01103; 1POM.  
 DR TRANSFAC: T02926; -  
 DR Mendel: 24821; Antma; MYB; 24821.  
 DR InterPro: IPR001005; MYB\_DNA\_bind.  
 DR Pfam: PF00249; MYB\_DNA-binding; 2.  
 DR SMART: SM00395; SANT; 2.  
 DR PROSITE: PS00037; MYB\_1; 1.

DR PROSITE; PS00334; MYB\_2; 1.  
 DR PROSITE; PS50090; MYB\_3; 2.  
 KW Nuclear protein; DNA-binding; Repeat; Transcription regulation.  
 FT DNA\_BIND 62 102 MYB.  
 FT DNA\_BIND 232 AA; 26164 MW; 883943FCBOD403D4 CRC64;  
 SQ SEQUENCE

Query Match 44.5%; Score 704.5; DB 10; Length 232;  
 Best Local Similarity 52.4%; Pred. No. 8.5e-54;  
 Matches 150; Conservative 24; Mismatches 55; Indels 57; Gaps 8;

QY 1 MGRSPCCCKAHTNKGAWTKEEDQRLINIRVHGGCGRSLPKAAGLRCGKSCRLRWINY 60  
 DB 1 MGRSPCCCKAHTNKGAWTKEEDQRLINIRVHGGCGRSLPKAAGLRCGKSCRLRWINY 60  
 QY 61 LRPDLKRGNTFEEDLILKLSLGNKWSLAGRLPGRTDNEIKYWNTHIKRKLISRG 120  
 DB 61 LRPDLKRGNTFEEDLILKLSLGNKWSLAGRLPGRTDNEIKYWNTHIKRKLISRG 120  
 QY 121 IDPQTHREPLNO-TANTNTYTAPELDFRNSPTSVSKSSSIKNPSLDNFYNEQFKNSTDS 179  
 DB 121 IDPQTHREPLNO-TANTNTYTAPELDFRNSPTSVSKSSSIKNPSLDNFYNEQFKNSTDS 179  
 QY 180 LEEPCATSSGWTDEEOEOLHKQOYGPSNGO--DINELSIGIVSADSSRYSNANSA 237  
 DB 150 KEE-----DTKKKAVNDIKEENSFYQERCPDLNLDKLT---SPCOQOQINTHYE 197  
 QY 238 ESKPKVNNNNFOLEQAMVAKAVCLQWLGFGTSEICRNCQNSN 283  
 DB 198 NKTGCRNG-----SSTLCFVCRLGIONSKDC-SCSDGVGN 232

RESULT 11  
 ID 0957Y2 PRELIMINARY; PRT; 246 AA.  
 AC 0957Y2  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE PUTATIVE DNA BINDING PROTEIN.  
 GN F12K8.1 OR MYB3.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Federgruel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,  
 RA Altafi H., Araujo R., Huizar L., Kowley D., Buehler E., Dunn P.,  
 RA Gonzalez A., Krementseva I., Kim C., Lenz C., Li J., Liu S.,  
 RA Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaya V.S.,  
 RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.,  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 RT [2]  
 RT "Towards functional characterisation of the members of the R2R3-MYB  
 gene family from Arabidopsis thaliana."  
 RA Kitzman H.D., Denekamp M., Greco R., Jin H.-L., Leyva A., Weissner R.,  
 RA Petroni K., Urzabugu A., Bevan M., Martin C., Smeekens S.,  
 RA Tonelli C., Paz-Ares J., Weissshaar B.;  
 RA "Towards functional characterisation of the members of the R2R3-MYB  
 gene family from Arabidopsis thaliana."  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLUMBIA;  
 RX MEDLINE=99056848; PubMed=9839469;  
 RA Kitzman H.D., Denekamp M., Greco R., Jin H.-L., Leyva A., Weissner R.,  
 RA Petroni K., Urzabugu A., Bevan M., Martin C., Smeekens S.,  
 RA Tonelli C., Paz-Ares J., Weissshaar B.;  
 RA "Towards functional characterisation of the members of the R2R3-MYB  
 gene family from Arabidopsis thaliana."  
 DR HSSP; P01103; 1POM.  
 DR InterPro; IPR001005; MYB\_DNA\_bind.  
 DR Pfam; PF00249; MYB\_DNA-binding; 2.  
 DR SMART; SM00395; SANT; 2.  
 DR PROSITE; PS00037; MYB\_1; UNKNOWN\_1.  
 DR PROSITE; PS00334; MYB\_2; 1.  
 DR PROSITE; PS00334; MYB\_2; 1.

DR PROSITE; PS50090; MYB\_3; 2.  
 SQ SEQUENCE 246 AA; 28151 MW; 2CA8A529153FF486 CRC64;

Query Match 44.3%; Score 702; DB 10; Length 246;  
 Best Local Similarity 54.08%; Pred. No. 1.5e-53;  
 Matches 149; Conservative 33; Mismatches 52; Indels 42; Gaps 7;

QY 13 NKGATKEEQRLINIRVHGGCGRSLPKAAGLRCGKSCRLRWINYLRPDLKRGNTFE 72  
 DB 2 NKGATKEEQRLINIRVHGGCGRSLPKAAGLRCGKSCRLRWINYLRPDLKRGNTFE 61  
 QY 73 EEDLILKLSLGNKWSLAGRLPGRTDNEIKYWNTHIKRKLISRGIDPQTHREPLNO 132  
 DB 62 EEDLILKLSLGNKWSLAGRLPGRTDNEIKYWNTHIKRKLISRGIDPQTHREPLNO 120  
 QY 133 ANNTNTYTAPELDFRNSPTSVSKSSSIKNPSLDNFYNEQFKNSTDSLEP-----NCTA 187  
 DB 121 -----SVSPSSLDNDVETLHLDSPGVKPPVPEEIGMANNCE 160  
 QY 188 SSGATDEEOEOLHKQOYGPSNGQDINELSIG-IVSADSSR-VSNANSAESKPKVDN 245  
 DB 161 SSGATSEKD-----YNEEDWVNLDELSTGSPSYESTRKYSVDSASTRWMS 210  
 QY 246 NNEQLEQAMVAKAVCLQWLGFGTSEICRNCQNSN 281  
 DB 211 ELF-----GAHSDAVCLCGRIGLFRNESCRCNCRVSD 242

RESULT 12  
 ID 095M28 PRELIMINARY; PRT; 274 AA.  
 AC 095M28  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE DNA-BINDING PROTEIN.  
 GN MYB32.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=LANDSBERG ERECTA;  
 RA Li S.F., Heazlewood J., Parish R.W.,  
 RT "Cloning of three MYB-like genes from Arabidopsis thaliana (Accession  
 RT Nos. U26933, AF048841, and U26934) (FGR99-138).";  
 RL Plant Physiol. 121:313-313(1999).  
 DR EMBL; U26933; AAF13100.1;  
 DR HSSP; P01103; 1POM.  
 DR InterPro; IPR001395; Aldo\_ket\_red.  
 DR InterPro; IPR001005; MYB\_DNA\_bind.  
 DR Pfam; PF00249; MYB\_DNA-binding; 2.  
 DR SMART; SM00395; SANT; 2.  
 DR PROSITE; PS00063; ALDO-KETO\_REDUCTASE\_3; UNKNOWN\_1.  
 DR PROSITE; PS00037; MYB\_1; 1.  
 DR PROSITE; PS00334; MYB\_2; 1.  
 DR PROSITE; PS50090; MYB\_3; 2.  
 KW DNA-binding.  
 SQ SEQUENCE 274 AA; 31465 MW; 6C06ACB15D794CAC CRC64;

Query Match 43.2%; Score 684; DB 10; Length 274;  
 Best Local Similarity 49.5%; Pred. No. 6.3e-52;  
 Matches 146; Conservative 30; Mismatches 61; Indels 58; Gaps 9;  
 QY 1 MGRSPCCCKAHTNKGAWTKEEDQRLINIRVHGGCGRSLPKAAGLRCGKSCRLRWINY 60  
 DB 1 MGRSPCCCKAHTNKGAWTKEEDQRLINIRVHGGCGRSLPKAAGLRCGKSCRLRWINY 60  
 QY 61 LRPDLKRGNTFEEDLILKLSLGNKWSLAGRLPGRTDNEIKYWNTHIKRKLISRG 120

Db 61 LRPDLKRGNFLEEDDLIIKLSLGNKWSLIAFRLPGRTDNEIKYWNTHIKRLLRG 120  
 QY 121 IDPQTHRLNQTANTNTVTAPELDFRNSPTSVSKSSIKPISLDFNYNEQFKNSTDSL 180  
 Db 121 IDPQTHRLNQTANTNTVTAPELDFRNSPTSVSKSSIKPISLDFNYNEQFKNSTDSL 158  
 QY 181 EEPNCTASSGMTDEEQOELHKKOQYGPSNQ--DINLELSIGIVSADSSRVSNANSAE 238  
 Db 159 EK--IANFG-----DERIQKREYSVVEERCLDNLLELRISPPWODKLFH----- 200  
 QY 239 SKPVDNNNFOLFQAMAVAKVCLCMQLGFTSEICRNCN-----SNSNGFYS 287  
 Db 201 -----DERNLRFGR-----VKHRCACRFGFGNGKEC-SCNNVKQOTEDSSSSSYS 245

RESULT 13

ID 049608 PRELIMINARY: PRT: 274 AA.  
 AC 049608;  
 DT 01-JUN-1998 (TREMBlrel. 06, Created)  
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE MYB-LIKE PROTEIN (MYB-LIKE PROTEIN).  
 GN MYB OR MAE13.50 OR AY4634950.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC Eucosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Beyer K.F., Purnelle B., Boutry M., Goffeau A., Hohenseel J., Mewes H.W.,  
 RA Mayer K.F.X., Schueller C.;  
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Murphy G., Ridley P., Hudson S., Mewes H.W., Lemcke K., Mayer K.F.X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Purnelle B., Boutry M., Goffeau A., Mewes H.W., Lemcke K.,  
 RA Mayer K.F.X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL022023; CA11764.1; -;  
 DR EMBL; AL161586; CAB80216.1; -;  
 DR HSSP; P01103; IPOM.  
 DR Mendel; 28225; Arabid.MYB:28225.  
 DR InterPro; IPR001395; AIGO\_ket\_red.  
 DR InterPro; IPR001005; MYB\_DNA\_bind.  
 DR Pfam; PF00249; MYB\_DNA\_bind.  
 DR SMART; SM00395; SANT; 2.  
 DR PROSITE; PS00063; ALDOXETO\_REDUCTASE\_3; UNKNOWN\_1.  
 DR PROSITE; PS00037; MYB\_1; 1.  
 DR PROSITE; PS00334; MYB\_2; 1.  
 DR PROSITE; PS00090; MYB\_3; 2.  
 DR PROSITE; PS50090; MYB\_3; 2.  
 SQ SEQUENCE 274 AA; 31457 MW; 817C0609F7DB5517 CRC64;

Query Match 43.2%; Score 684; DB 10; Length 274;  
 Best Local Similarity 49.5%; Pred. No. 6.3e-52;  
 Matches 146; Conservative 30; Mismatches 61; Indels 58; Gaps 9;

QY 1 MGRSPCCERAHNTKGAATKEEDQRLINIRYHGECCWRSLEPRAAGLLRCGKSCRLRWNY 60  
 Db 1 MGRSPCCERAHNTKGAATKEEDQRLINIRYHGECCWRSLEPRAAGLLRCGKSCRLRWNY 60  
 QY 61 LRPDLKRGNFTEEDDLIIKLSLGNKWSLIAFRLPGRTDNEIKYWNTHIKRLLRG 120  
 Db 61 LRPDLKRGNFTEEDDLIIKLSLGNKWSLIAFRLPGRTDNEIKYWNTHIKRLLRG 120

Db 61 LRPDLKRGNFTEEDDLIIKLSLGNKWSLIAFRLPGRTDNEIKYWNTHIKRLLRG 120  
 QY 121 IDPQTHRLNQTANTNTVTAPELDFRNSPTSVSKSSIKPISLDFNYNEQFKNSTDSL 180  
 Db 121 IDPQTHRLNQTANTNTVTAPELDFRNSPTSVSKSSIKPISLDFNYNEQFKNSTDSL 158  
 QY 181 EEPNCTASSGMTDEEQOELHKKOQYGPSNQ--DINLELSIGIVSADSSRVSNANSAE 238  
 Db 159 EK--IANFG-----DERIQKREYSVVEERCLDNLLELRISPPWODKLFH----- 200  
 QY 239 SKPVDNNNFOLFQAMAVAKVCLCMQLGFTSEICRNCN-----SNSNGFYS 287  
 Db 201 -----DERNLRFGR-----VKHRCACRFGFGNGKEC-SCNNVKQOTEDSSSSSYS 245

RESULT 14

ID 023889 PRELIMINARY: PRT: 239 AA.  
 AC 023889;  
 DT 01-JAN-1998 (TREMBlrel. 05, Created)  
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE OSMYB1.  
 GN OSMYB1.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE-SEED;  
 RC MEDLINE=98036074; PubMed=9370307;  
 RX Suzuki A., Suzuki T., Tanabe F., Toki S., Washida H., Wu C.-Y.,  
 RA Takaiwa F.;  
 RL Cloning and expression of five myb-related genes from rice seed.  
 RT Gene 198:393-398(1997).  
 RL EMBL; D88617; BAA23337.1; -;  
 DR HSSP; P01103; IPOM.  
 DR TRANSFAC; T02869; -;  
 DR Mendel; 24458; Oryza.MYB:24458.  
 DR InterPro; IPR001005; MYB\_DNA\_bind.  
 DR Pfam; PF00249; MYB\_DNA\_binding; 2.  
 DR SMART; SM00395; SANT; 2.  
 DR PROSITE; PS00037; MYB\_1; UNKNOWN\_1.  
 DR PROSITE; PS00334; MYB\_2; 1.  
 DR PROSITE; PS50090; MYB\_3; 2.  
 SQ SEQUENCE 239 AA; 26725 MW; B937E5E7848826F4 CRC64;

Query Match 43.1%; Score 683; DB 10; Length 239;  
 Best Local Similarity 93.0%; Pred. No. 6.6e-52;  
 Matches 120; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGRSPCCERAHNTKGAATKEEDQRLINIRYHGECCWRSLEPRAAGLLRCGKSCRLRWNY 60  
 Db 1 MGRSPCCERAHNTKGAATKEEDQRLINIRYHGECCWRSLEPRAAGLLRCGKSCRLRWNY 60  
 QY 61 LRPDLKRGNFTEEDDLIIKLSLGNKWSLIAFRLPGRTDNEIKYWNTHIKRLLRG 120  
 Db 61 LRPDLKRGNFTEEDDLIIKLSLGNKWSLIAFRLPGRTDNEIKYWNTHIKRLLRG 120  
 QY 121 IDPQTHRL 129  
 Db 121 IDPQTHRL 129

RESULT 15  
 ID 042379 PRELIMINARY: PRT: 269 AA.  
 AC 042379;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

01-JUN-2001 (TRENBLrel. 17, last annotation update)  
 DE Y49 GENE.  
 GN MYB OR Y49 OR T24121.13.  
 OS Arabidopsis thaliana (Mouse-ear cross).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Quedvlieg N.E.M., Dockx J., Keultjes G.G.M., Smeekens J.C.M.;  
 RL Submitted (Aug-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LANDSBERG ERECTA;  
 RX MEDLINE=96132152; PubMed=8580966;  
 RA Li S.F., Parish R.W.;  
 RT Isolation of two novel myb-like genes from Arabidopsis and studies on  
 the DNA-binding properties of their products.\*;  
 RL Plant J. 8:963-972(1995).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LANDSBERG ERECTA;  
 RA Heazlewood J.L.;  
 RL Submitted (May-1995) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. COLUMBIA;  
 RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., Vanaken S.E.,  
 Barnstead M.E., Mason T.M., Bowman C.L., Rongling C.M., Benito M.,  
 Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.;  
 RA Fraser G.M., Venter J.C.;  
 RT Arabidopsis thaliana chromosome II BAC T24121 genomic sequence.\*;  
 RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: X90385; CAA62033.1; -;  
 DR EMBL: U26937; AAA98762.1; -;  
 DR EMBL: AC005825; AAD24605.1; -;  
 DR HSSP: P01103; 1POM.  
 DR TRANSFAC: T02540; -;  
 DR Mendel: 6896; Arabidopsis: MYB\_6896.  
 DR InterPro: IPR001005; Myb\_DNA\_bind.  
 DR Pfam: PF00249; myb\_DNA-binding; 2.  
 DR SMART: SM00395; SANT; 2.  
 DR PROSITE: PS00037; MYB\_1; 1.  
 DR PROSITE: PS00334; MYB\_2; 1.  
 DR PROSITE: PS00090; MYB\_3; 2.  
 KW DNA-binding.  
 SO SEQUENCE 269 AA; 31009 MW; 7A6C5D7C3CA0135C CRC64;

Query Match 43.0%; Score 681.5; DB 10; Length 269;  
 Best Local Similarity 48.8%; Pred. No. 1e-51;  
 Matches 142; Conservative 35; Mismatches 59; Indels 55; Gaps 8;

OY 1 MGRSPCCERAKHTNKGAMTKEEDORLINIYRVHGGCWRSLPKAGLLRCGKSCRLRWINY 60  
 DB 1 MGRSPCCERAKHTNKGAMTKEEDORLINIYRVHGGCWRSLPKAGLLRCGKSCRLRWINY 60  
 OY 61 LRPDLKRGNTFEEDLLIKLHSLGKMSLIAGRLPGRTDNEIKNYWNTHIKRLKLSRG 120  
 DB 61 LRPDLKRGNTFEEDLLIKLHSLGKMSLIAGRLPGRTDNEIKNYWNTHIKRLKLSRG 120  
 OY 121 IDPOTHRPLNOTANTWTVAPELDFNSPTSVSKSSIKNPSLDFNNEFOKSNTOSL 180  
 DB 121 IDPOTHRPLNOTANTWTVAPELDFNSPTSVSKSSIKNPSLDFNNEFOKSNTOSL 180  
 OY 181 EEPNCTASGAMTTDEPO---OEQLHKQOYGPSNGODINLELSIGIVASADSSRVANSANA 237  
 DB 163 OKONKTIYRNGLVCKEERVVVEEKI-----GPDNLLELRISPPWQNGREISTCTAS 212  
 OY 238 ESKPKYDNNNFOLFEOAMAKAVCLCWLQFGTSEICRNCQNSNSNGFYSY 288  
 DB 213 RF-----YEMNDMEC-----SSETYK-CQTESSSI-SY 239

Search completed: January 23, 2002, 21:21:03  
 Job time: 565 sec